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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compound containing protein from TGF-beta superfamily - has bone and/or cartilage inducing activity, useful in treatment of, e.g. osteoporosis, bone damage, Paget's disease and osteoarthritis claim 3; Page 9; 10pp; German Transforming growth factor (TGF)-beta protein designated MP52. MP52 can be used in a compound of formula (I):

A.X(1-20)-8(1-20) MP52 can be used to regenent, of the TGF-beta superfamily with cartilage and/or bone inducing activity (e.g. MP52);

B. 1 or more substituent groups with an affinity to the extracellular matrix, cellular components of bone and/or cartilage and/or to a biocompatible carrier matrix: X = 1 or more covalent bonds and/or spacer treat bone or cartilage related disorders, including osteoporosis, Paget's disease, osteodystrophy, osteoarthritis or osteoarthropathy and
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Human TGF-beta protein MP52.
Human transforming growth factor-beta; TGF-beta; MP52; superfamily;
Joartilage; bone inducing activity; inhibit; bone resorption.
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                     Score 3662; DB 1; I
Pred. No. 0.00e+00;
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W19210 standard; Protein; 501
                     / Match 100.0%;
Local Similarity 100.0%;
nes 501; Conservative
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22-DEC-1995; 048476.
22-DEC-1995; DE-048476.
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N-PSDB; T69695.
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DE19548476-A1.
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 cartilage damage caused by wounding or overloading
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                                                                                           1 MRLPKLLTFLLWYLAWLDLEFICTVLGAPDLGQRPQGTRPGLAKAEAKERPPLARNVFRP
                                                                                                          GGHSYGGGATNANARAKGGTGQTGGLTQPKKDEPKKLPPRPGGPEPKPGHPPQTRQATAR
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                                   Score 3662; DB 1;
Pred. No. 0.00e+00;
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378. .381
/note= "Proteolytic procession"
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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/note= "Signal peptide"
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189. .19
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07-NOV-1994; U12814.
07-NOV-1994; WO-U128
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                                                                          The sequence represents human articular cartilage-derived
The sequence represents human articular cartilage-derived
morphogenetic protein-1 (CDMP-1). The protein contains a putative
transmembrane signal peptide, a pro-region, a typical proteolytic
cleavage site, and a C-terminal domain containing 7 highly
conserved Cys residues characteristic of the transforming growth
caserved Cys residues characteristic of the transforming growth
caserved Cys residues characteristic of the transforming growth
caserved Cys residues A 13-amino-acid peptide (R95642) has been used
in the pro-region. A 13-amino-acid peptide (R95642) has been used
conserved main-antibodies for screening of tissues for
CDMP-1 expression. A consensus highly conserved motif in CDMP
proteins (R95641) is present in the C-terminal domain. CDMP-1 is
present in a purified cartilage extract (claimed) which stimulates
local cartilage formation and repair when combined with a matrix
and implanted in a mammal. The protein may be used in therapy of
e.g. chondromalacia or osteoarthritis, to heal joint surfaces, or
to repair cartilage after reconstructive surgery.
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15-MAR-1995 (first entry)
15-MAR-1995 (first entry)
GDP-5; growth differentiation factor 5; diagnostic; therapeutic;
detection; treatment; cell proliferative disorders; uterus tissue;
skeletal tissue; uterine acoplasm; endometriosis; reagent;
skeletal tissue; transforming growth factor beta superfamily; TGF beta.
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                                        proteins in vivo.
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                                    New purified cartilage extracts and development and repair of cartilage Claim 11; Fig 1; 34pp; English.
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98.4%;
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96-251714/25.
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N-PSDB; T31601
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R60022 shows the amino acid sequence of Growth differentiation factor 5, which is encoded by Q70010. The GDF-5 sequence contains a core of hydrophobic amino acids near the N-terminus, suggestive of signal sequence secretion. The sequence contains all of the highly conserved residues present in other members of the Transforming growth factor beta superfamily, including the seven cysteine residues with their characteristic spacing. The prods of the invention can be used for detection of a cell poliferative disorder of the uterus or skeletal tissue which is associated with GDF-5 expression, whitseness sequences of GDF-5 can be used to treat uterine expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGHIYGVGATNA--RAKGSSGQT----QAKKDEPRKMPPRSGGSETKPGPSSQTRQAAAR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRLPKLLTLLLWHLAWLDLELICTVLGAPDLGQRTPGAKPGLTKAEAKERPPLARNVFRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neoplasm, endometriosis, or skeletal disorders (claimed). The prods can also be used in eg. contraception, in vitro fertilisation or in
                                                                                                                  /note= "putative tetrabasic proteolytic processing
                                                                                                                                                                                         /note= "putative tetrabasic proteolytic processing
                                                                                                                                                                                                                                                                                  12-JAN-1994; U00657.
12-JAN-1993; US-003144.
(UVJO ) UNIV JOHNS HOPKINS SCHOOL MED.
HUNDH T, Lee S;
WPI: 94-249127/30.
N-PSDB; Q70010.
New growth differentiation factor-5 - used to develop prods. for the detection or treatment of cell proliferative disorders of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVTPKGQLPGGKASSKAGSAPSSFLLKKTREPGTPREPKEPFRPPPITPHEYMLSLYRTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILRKKPLDVAKPAVPSSGRVAQLKLSSCPSGRQPAALLDVRSVPGLDGSGWEVFDIWKLF
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                 /note= "potential glycosylation site"
371. .375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 9.21e-297;
23; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 3332; DB 1; I Pred. No. 9.21e-297;
                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preventing premature labour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 91.0%;
Best Local Similarity 91.2%;
Matches 457; Conservative
                                                                                                                                                                  .385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uterus or skeletal tissue
                                                                                                                                                                                                                     site"
                                                                                                                                                site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              495 AA;
                                                                                             cleavage_site
                                        modified_site
                                                                                                                                                                    cleavage_site
musculus.
                                                                                                                                                                                                                                                                  21-JUL-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used in tissue and wound repair, in treatment of bone, cartilage and tooth defects, and antibodies for diagnosis
Claim 11; Page 19; 29pp; English.

The sequences given in R4080 and R45447 represent framents of embryo and liver derived human transforming growth factor-beta (FGF-beta) respectively. The full length protein may be used in a pharmaceutical composition for the treatment of various bone, cartilage or tooth defects and in tissue and wound repair processes. These proteins may also be used as immunosuppressors in organ transplants and in cosmeric surgery. Antibodies raised against these proteins may be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFRPPPITPHEYMLSLYRTLSDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPVVRKQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RYVFDISALEKDGLLGAELRILRKKPSDTAKPAAPGGGRAAQLKLSSCPSGRQPASLLDV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGGPEPKPGHPPQTRQATARTVTPKGQLPGGKAPPKAGSVPSSFLLKKAREPGPPREPKE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                         pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFRPPFITPHEYMLSLYRTLSDADRKGGNSSVKLEAGLANTITSFIDKGODDRGPVVRKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSVPGLDGSGWEVFDIWKLFRNFKNSAQLCLELEAWERGRAVDLRGLGFDRAARQVHEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                             cartilage; tooth; wound repair; immunosuppressor; transplant; cosmetic surgery; antibody; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New transforming growth factor-beta family proteins
                                                                                                                                                                                                                                                           TGF-beta-like clone MP-52 protein.
Human; transforming growth factor; beta; TGF-beta;
bone; cartilage; tooth; wound repair; immunosuppres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 401
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                                                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-1993.
12-FBB-1993; E00350.
12-FBB-1993; ED-10234.
(BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL. Hoetten 6, Neidhardt H; WPI: 93-272824/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2925; DB 1; 1
Pred. No. 2.39e-258;
0; Mismatches 0;
                                                                                                                                                                        ¥.
SANNVYKQYEDMVVESCGCR 495
                             481 SANNVVYKQYEDMVVESCGCR 501
                                                                                                                                        T 11
R40800 standard; Protein; 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 79.9%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                        TGF-beta-like clone MP-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
WO9316099-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401;
                                                                                                                                                                                                                             11-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                             R40800;
                                                                                                                                                                                                                                                                                                                                              organ
475
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R95636 standard; Protein; 436 R95636; 25-OCT-1996 (first entry)

RESULT

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New purified cartilage extracts and proteins - used to stimulate the development and repair of cartilage in vivo.

The development and repair of cartilage in vivo.

Claim 11; Fig 2; 34pp; English.

The sequence represents cattle articular cartilage-derived morphogenetic protein-2 (CDMP-2). The N-terminal methionine and signal peptide is missing, but part of the pro-region, a typical proteolytic cleavage site and a C-terminal domain containing 7 highly conserved Cys residues characteristic of the transforming growth factor-beta gene family are present. A single N-91ycosylation site is located in the pro-region. A consensus highly conserved compile in CDMP proteins (R95641) is present in the C-terminal domain.

CDMP-2 is present in a purified cartilage extract (claimed) which a matrix and implanted in a mammal. The protein may be used in therapy of e.g. chondromalacia or osteoarthritis, to heal joint surfaces, or sequence 436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRPPQQPEAREPPGRGPRLVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDR 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 VAPAA---GSA-E-PGPAGAPRPGWEVFDVWRGLRP-QPWKQLCLELRAAWGGEPGAAED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARTPGPQQPPPDLRSLGFGRRVRTPQERALLVVFSRSQRKTLFAEMREQLGSATEVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E-R--G--RAV--DLRGLGFDRAARQVHEKALFLVFGRTKKRDLF-----F-N--EIKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 PGGGAEGSGPPPPPPPPPPPSGTPDAGLWSPSPGRRRRTAFASRHGKRHGKRSRLRCSKKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 RSG-QDDK------TVY-EY-LFSQR--RKRRAPLATRQGKRPSKNLKARCSRKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 LHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 SCPSGRQPASLLDVRSVPGLDGSGWEVFDIWKLFRNFKNSAQLCLEL-EAW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 54;
Cartilage-derived morphogenetic protein-2. cLowp-2; cattle, cartilage-derived morphogenetic protein-2; cDwp-2; carticular cartilage; chondrogenic; vulnerary; implantation; chondromalacia; osteoarthritis; therapy; joint repair.
                                                                                                                                                                                                                                                                                                                                                                                  352. .382
/note= "Consensus conserved motif (R95641)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 939; DB 1; Len
Pred. No. 2.00e-72;
...matches 69;
                                                                                                                                                                                                                                                                                                                                                           "C-terminal mature domain"
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                                                                                                                                                                                                                                                                                                      "Proteolytic processing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                       Location/Qualifiers
                                                                                                                                                                 l. .312
'note= "Pro-region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chang SC, Luyten FP, Moos M;
WPI; 96-251714/25.
                                                                                                                                                                                                                                                                                                           /rote= "C-+
352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.6%;
Best Local Similarity 47.6%;
Matches 189; Conservative
                                                                                                                                                                                                                                                                       .316
                                                                                                                                                                                                                 .91
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07-NOV-1994; U12814.
07-NOV-1994; WO-U12814.
                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                      /note=
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                                                                                                                                                                                                                 modified_site
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                                                                                                           Bos taurus.
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Inducing tendon and ligament formation using BMP-12, BMP-13 or MP-52 resetul for tissue healing and repair, treatment of tendonitis, improving flatation of tendons to bone etc.

Claim 5; Column 57-66; 438p; English.

Claim 5; Column 57-66; 438p; English.

Claim 5; Column 77-66; 438p; English.

Claim 6; Column 77-66; 438p; English.

Claim 6; Column 77-66; 438p; English.

Claim 6; Composition containing at least one protein selected from BMP-13, composition containing at least one protein selected from BMP-13, composition containing at least one protein selected from English.

CMP52 (see W2659) and BMP-12 (see W26589). The method is used for tissue (including skin) healing and repair. This is useful for treating tendonitis, carpal tunnel syndrome and other defects of traumatic or congenital origin, in cosmetic surgery and to improve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 APLATROGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHL 60
                                                         Example; projective proteins -12 and -13 and corresp. DNA - used in compsn. for inducing tendon/ligament-like tissue formation example; page 51-52; 84pp; English.

Example; Page 51-52; 84pp; English.

Oligos #6 and #7 (096218 6 096219) are used as primers for the amplification of a 275 bp DNA probe, the internal 269 bp of which corresp. to nts #607 to #865 of 096207, from the BMP-12 encoding plasmid subclone PCR1-12. This probe was radioactively labelled and used to screen a murine genomic library. DNA sequence analysis of one of positively hybridisting recombinants named MYR21 andicates that it encodes a portion of the mouse gene corresp. to the PCR product mV9 (murine homolog of the MP-52 sequence 096209/R78731).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human bone morphogenetic protein BMP-13.
BMP-13; bone morphogenetic protein; human; tendon; ligament;
wound healing; tissue repair; tendonitis; carpal tunnel syndrome;
                                                                                                                                                                                                                                                                                                                                                        Score 904; DB 1; Length 120; Pred. No. 3.33e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thomsen GH,
                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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/label=_Sig_peptide
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(HARD ) HARVARD COLLEGE.
Celeste AJ, Melton DA, Rosen VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .T 15
W26591;
W26591;
21-JAN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                    y Match 24.7%;
Local Similarity 100.0%;
hes 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-DEC-1993; 164103.
22-DEC-1994; US-362670.
07-DEC-1993; US-164103.
25-MAR-1994; US-217780.
02-NOV-1994; US-333576.
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WPI; 97-424270/39.
                    WPI; 95-224320/29.
N-PSDB; Q96209.
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N-PSDB; T90386
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  Wozney JM;
                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inducing formation of tendon and/or ligament tissues involves the administration of a composition containing at least one protein selected from MP52, BMP-12 (see W26589) and BMP-13 (see W26591). The method is used for tissue (including skin) healing and repair. This is useful for treating tendonitis, carpal tunnel syndrome and other defects of traumatic or congenital origin, in cosmetic surgery and to improve fixation of tendons or ligaments to bone. The specified proteins can also be used to increase activity of other BMPs e.g. BMP-2 (see W26597).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 EPTNHAVIQTLANSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 APLATROGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MP-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                           Human MP52 protein.
MP52; BMP; bone morphogenetic protein; human; tendon; ligament;
wound healing; tissue repair; tendonitis; carpal tunnel syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI: 97-424270/39.
Inducing tendon and ligament formation using BMP-12, BMP-13 or M rescul for tissue healing and repair, treatment of tendonitis, improving fixation of tendons to bone etc Claim 5; Column 39-40; 43pp; English.
This polypeptide comprises human MP52. A claimed method for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wolfman NM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 24.7%; Score 904; DB 1; Length 120; Best Local Similarity 100.0%; Pred. No. 3.33e-69; Ltches 120; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bone morphogenetic protein; MP52; tendon; ligament.
Mus musculus.
WO9516035-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEMY ) GENETICS INST INC.
(HARD ) HARVARD COLLEGE.
Celeste AJ, Melton DA, Rosen VA, Thomsen GH,
                                                                                                                                                                                                                                           Location/Qualifiers
                                                           W26590 standard; Protein; 120 AA
                                                                                                                                                                                                                                                                  1. .120
/note= "Claim 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R78731 standard; Protein; 120 AA
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/note= "Claim 5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-NOV-1995 (first entry) Murine protein MP52.
                                                                                                         21-JAN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-1995.
06-DEC-1994; U14030.
07-DEC-1993; US-164103.
25-MAR-1994; US-217780.
02-NOV-1994; US-333576.
                                                                                                                                                                                                                                                                                                                                                                                                                    | 22-DEC-1994; US-362670. 
07-DEC-1993; US-164103. 
25-MAR-1994; US-217780. 
02-NOV-1994; US-333576.
                                                                                                                                                                                                                                                                                                                                                                                                 164103
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07-DEC-1993;
                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                      US5658882-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                             Protein
                                                                                    W26590;
                                                                                                                                                                                                    therapy
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Wolfman NM;

R78731;

RESULT

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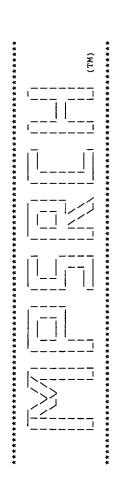
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Gaps 22;
                                                                                                                                                        62 -LLDARTLDPOGAPPAGWEVFDVWQGLRH-QPWKOLCLELRAAWGELDAGEARARGPQ 119
11| |:: | | :||||||:| | | |:|:
276 SLLDVRSV-P-GLDGSGWEVFDIWKLFRNFKNSAQLCLEL-EAW-----E-RGRAV- 322
                                                                                                                                                                                                                                                       fixation of tendons or ligaments to bone. The specified proteins can also be used to increase activity of other BMPs e.g. BMP-2 (see W26597).
                                                           Score 903; DB 1; Length 321;
Pred. No. 4.12e-69;
61; Mismatches 46; Indels 46;
                                                                                                                                                                                                                                                                                                                                                     300 DAGNNVYKQYEDMVVESCGCR 321
                                                                                                                                                                                                                                                                                                                                                                  480 DSANNVYKQYEDMVVESCGCR 501
                                                           Query Match 24.7%;
Best Local Similarity 52.5%;
Matches 169; Conservative
                                   321 AA;
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Search completed: Wed Apr 19 19:52:00 2000 Job time : 115 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Wed Apr 19 19:44:13 2000; MasPar time 96.72 Seconds 359.134 Million cell updates/sec Run on:

lar output not generated.

>US-09-297-092-1 (1-501) from US09297092.pep 3662 1 MRLPKLLTFLLWYLAWLDLE......ANNVVYKQYEDMVVESCGCR 501 ritle:

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

225878 seqs, 69334122 residues

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptremb112
1:sp_archea 2:sp_bacteria 3:sp_fung1 4:sp_human
5:sp_invertebrate 6:sp_mamma1 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 49.475; Variance 95.258; scale 0.519 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	% Query Match Length	DB	13	Description	Pred. No.
1	2555	69.8	200	13	Q9W6G	GDF-5 PROTEIN.	0.00e+00
7	2055	56.1	324	13	09 X HW9	GROWTH DIFFERENTIATION	0.00e+00
m	1451	39.6	257	7	042303	SONTACT (FRAGMENT).	2.32e-276
4	1278	34.9	399	h	004F55	GROWTH AND DIFFERENTIA	1.07e-238
5	1200	32.8	412	13	012938	DYNAMO PROTEIN PRECURS	8.86e-222
9	822	22.4	126	13	093573	PUTATIVE GROWTH/DIFFER	1.45e-140
7	813	22.2	261	13	Q9W6C0	GROWTH/DIFFERENTIATION	1.19e-138
80	585	16.0	417	S	09xx07	BONE MORPHOGENETIC PRO	9.62e-91
6	553	15.1	204	Ŋ	69ZX60	BONE MORPHOGENETIC PRO	3.98e-84
10	551	15.0	191	Ŋ	026468	TRANSFORMING GROWTH FA	1.03e-83
11	551	15.0	411	13	093369	BONE MORPHOGENETIC PRO	1.03e-83
12	546	14.9	361	Ŋ	096504	BONE MORPHOGENETIC PRO	1.10e-82
13	545	14.9	453	13	P87373	BMP5.	1.77e-82
14	543	14.8	411	13	057573	BONE MORPHOGENETIC PRO	4.58e-82
15	536	14.6	178	S	025211	DECAPENTAPLEGIC (FRAGM	1.26e-80
16	534	14.6	400	13	057574	BONE GENETIC PROTEIN 4	3.25e-80
17	527	14.4	386	13	013109	BMP2.	8.92e-79
18	529	14.4	400	13	091703	PROTEIN 4.	3.46e-79
19	529	14.4	400	13	073818	BONE MORPHOGENETIC PRO	3.46e-79
20	526	14.4	424	13	Q9YGH7	OSTEOGENIC PROTEIN-1 H	1.43e - 78

2.30e-73 2.58e-75 4.36e-75 4.36e-75 4.36e-75 2.87e-74 7.35e-74 1.23e-72 1.23e-72 2.24e-69 9.13e-69 9.14e-68 1.56e-66 1.56e-66	1.73e-62 1.76e-61 1.82e-58 2.90e-57
BONE MORPHOGENETIC PROBMP4. MGDF PRECURSOR. BMP2-4. BONE MORPHOGENETIC PRODECAPENTAPLEGIC PROTEING. GROWTH FACTOR CVGI. HOMOLOG OF DPP SUBCLAS ANTI-DORSALIZING MORPH GROWTH DIFFERENTIATION BONE MORPHOGENETIC PROBENE MORPHOGENETIC PROBENE MORPHOGENETIC PROBECT PROTEING MORPHOGENETIC PROBENE MORPHOGENETIC PROFESSIONE GROWTH FARMED MORPHOGENETIC PROFESSIONE GROWTH FARMED MORPHOGENETIC PROFESSIONE MORPHO	GROWTH DIFFERENTIATION GROWTH DIFFERENTIATION GROWTH/DIFFERENTIATION DVR-1 (FRAGMENT).
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Glycoprotein.
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01-NOV-1999 (
01-NOV-1999 (
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Q9W753
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                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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                                                                                                                            SALEKDGLLGAELRVLRKKPSDAWK--SHSSGKTSQVKLFSCSTNRQAATLLDSRTVSIT 118
                                                                                                                                                                                                                                                                                                                                   MEDLINE; 99119368.
MERINO R., MACIAS D., GANAN Y., ECONOMIDES A.N., WANG X., WU Q., STAHL N., SAMPATH K.T., VARONA P., HURLE J.M.;
"Expression and function of Gdf-5 during digit skeletogenesis in the embryonic chick leg bud.";
Dev. Biol. 206:33-45(1999).
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          NEIKARSGODDKTVYEYLFNORRKRRAPLATROCKRPSKNLKPRCSRKALHVNFKDMGWD
                                                                                                                  DWIIAPLEYEAYHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITPHEYMLSLYRTLSDAERKGVNGSVKLEAGLANTITSFIDKGQDERAPTIRKQKYIFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIPKWEVFDIWKLFRNFKNLVNLCFELETFDRGRAVDLRTVGFNRTGRQVNEKALFLVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTKKRDLFFNEIKARSGQDDKTVYESLFNQRRKRRAPLATRQGKRPSKNLKARCSRKALH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNFKDMGWDDWIIAPLEYEAYHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCC
VAELRILRKNPSDTWK--SHSSGKTSOVKLFSCSTNROAATLLDSRTVSITDTPKWEVFD
                                     IWKLFRNFKNLVNLCFELETFDRGRAVDLRTVGFNRTGRQVNEKALFLVFGRTKKRDLFF
                                                                                                                                                                                                                                                                                                                                                                                             -i- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY. EMBL; AF075441; AAD14568.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
GROWTH DIFFERENTIATION FACTOR 5 PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2055; DB 13;
Pred. No. 0.00e+00;
34; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       324 324 37206 MW; E2CF56AC CRC32;
                                                                                                                                                                                                                   Ā
                                                                                                                                                                                                                   324
                                                                                                                                                                                                                                      Created)
                                                                                                                                                       ILFIDSANNVYKQYEDMVVESCGCR 500
                                                                                                                                                                  476 ILFIDSANNVYKQYEDMVVESCGCR 501
                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel, 10, 01-NOV-1999 (TrEMBLrel, 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.7%;
Matches 273; Conservative
                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                   P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            TISSUE-LEG BUD;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein.
NON_TER
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SEQUENCE
                                                                                                                                                                                                                             09YHW9;
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                  236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 RSGHDNKTVYEYLFTQRRMRRAPLP-R-GKKPIKNPKQRCNRKQLHVNFKEMGWDDWIIA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 PLEYEAFHCDGVCDFPIRSHLEPTNHAIIQTLMNSMDPRSTPPTCCVPTRLSPISILYID 236
                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ILRKKHMDSRK-ATFSEGMAV-LRLFTCASGKNAAVLLQARPFDSHSASYWEVFDIWKVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mech. Dev. 65:163-173(1997),
-1 - SINLIARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY EMBL; Y12005; CRA72733.1; -. HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRUNEAU S., MOURRAIN P., ROSA F.M.;
"Expression of contact, a new zebrafish DVR member, marks m cell lineages in the developing pectoral fins and head and regulated by retinoic acid.";
Mech. Dev. 65:163-173(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27; Indels
                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1451; DB 13;
Pred. No. 2.32e-276;
41; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6BDDCADC CRC32;
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                                                                                                                                           257
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                                                                                                                                                                                      Created)
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                                             492
                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contact.
1
257 PC
29787 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 SANNVYKOYEDMVVESCGCR 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 SANNVYKQYEDMVVESCGCR 257
                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZFIN; ZDB-GENE-990415-39; CC PROSITE; PS00250; TGF_BETA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.68;
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Matches 189; Conservative
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257 AA;
                                                                                                                                                                                                                                                     CONTACT (FRAGMENT).
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ETCGCR 126
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ESCGCR 501
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         Query Match
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093573
093573;
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                                                                                                                                                                        63 PAVVPHEYMLSIYKTFSTAEKLGINASFFQSSKSANTISSFVDRRRDNLSLPSLKRKKYL 122
                                                                                                                                                                                    123 FDVSTLSDKEELVGAELRVFRKAPVESAK - TPLD - LYNLQVTSCTSQAQLDYRTLDLR 178
                                                                                                                                                                                                                                                                 179 DTPS---PGWQVFDVWKSLQDISQGKKQICVELKAISLTTGLEVNLRSLGLARKPRSHQE 235
                                                                                                                                                                                                                                                                             236 KALLVVFTKSSRKNLY-NELKEQV-HSSKSMEKEARLHFKTRRRRTTFNSRHGKRHGRK 293
                                                                                                                                                                                                                                                                                                                           294 SRLRCSKKPLHVNFKELGWDDWIIAPLEYEAHHCEGVCDFPLRSHLEPTNHAIIQTLMNS 353
                                                                                                                                                                                                                                                                                                                                                                        396 LKARCSRKALHVUFKDMGWDDMIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLANS 455
                                                                                                                                                                                                                                TISSUB-WHOLE ENDAN N.A.

TISSUB-WHOLE EMBRYO;

MEDLINE; 97231294

"Dynamo, a new zebrafish DVR member of the TGF-beta superfamily is expressed in the posterior neural tube and is up-regulated by Sonic Mech. Dev. 61:199-212(1997).

"SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.

HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brachydanio rerio (Zebrafish) (Zebra danio).
Bukaryota: Metazoa: Chordata: Craniata: Vertebrata; Actinopterygii;
Neopterygii: Teleostei: Buteleostei: Ostariophysi: Cypriniformes;
Cyprinoidea: Cyprinidae: Rasborinae; Danio.
                   CHANG C., HEMMATI-BRIVANLOU A.;
"Xenopus GDF6, a new antagonist of noggin and a partner of BMPs Development 0:0-0(1999).
-! SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY. EMBL; AF155125; AAD38402.1; ...
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                        Score 1278; DB 13; Length 399;
Pred. No. 1.07e-238;
85; Mismatches 63; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                         012938;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DYNAMO PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
DYNAMO PROTEIN.
1E5AEE13 CRC32;
                                                                                                   399 AA; 45571 MW; 98A43227 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               412 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETEN; ZED-GENE-980526-442; dynamo.
PROSITE; PS00250; TGF_BETA; 1.
PFAM; PP00019; TGF-beta; 1.
PRAM; PR00688; TGFb_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
Signal; Glycoprotein.
Signal 293 412 DYNAMO P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293 412 D
412 AA; 47071 MW;
                                                                                                                        Query Match
Best Local Similarity 52.0%;
                                                                                                                                               180; Conservative
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        SEQUENCE FROM N.A.
                                                                                        Glycoprotein
SEQUENCE 3
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012938
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LEE K.J., MENDELSOHN M., JESSELL T.M.;
"Neuronal patterning by BMPs: A requirement for GDF7 in the generation of a discrete class of commissural interneurons in the mouse spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PLRSHLEPTNHAIIQTLMNSMDPESTPPSCCVPSKLSPISILYIDSGNNVVYKQYEDMVV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 AIEPHDYMISIYKTFSAAEKLGLNASFFRSSKAANTITSFVDEGODDHLNSPLWRQKYLF 131
                                                                                                                                                                                                 132 DVSTLSENVEILGAELRIY-TKISGSFRASETGPV-EIQL-LS-CQSHTVLDSQ-TL-DL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KSKSRCSKKPLHVNFRELGWDDWVIAPLDYEAYHCEGMCDFPLRSHLEPTNHAIIQTLMN 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                186 EDAHKPKWEVFDVWEIFKERQHHSHGNRFCLELRATLDNPEREIDLQYLGFHRHGRPQLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RRKRRTTIAARSGGRGHGKKAKTRCSRKPLHVNFKELGWDDWIIAPLDYEAYHCEGVCDF
                                                                                                                                                                                                                                                                                                                                                                                                       KAILVVFTRSKKRQSLFYEKREKIKLWGLDSIGKERRSHSKTRRSRRTALPNRHGKRHGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY. EMBL, AF089086; AAC97113.1; -. HSSP; P18075; IBMP. PROSITE; PS00250; TGF-BETA; 1. PROSITE; PS00250; TGF-BETA; 1. PF00019; TGF-beta; 1.
                                                 17;
  Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 126;
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PUTATIVE GROWTH/DIFFERENTIATION FACTOR 6/7 (FRAGMENT).
                                                 75; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 22.4%; Score 822; DB 13; 1
Best Local Similarity 79.4%; Pred. No. 1.45e-140;
Matches 100; Conservative 20; Mismatches 5;
Score 1200; DB 13;
Pred. No. 8.86e-222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER 1 1 SEQUENCE 126 AA; 14265 MW; 612DDD07 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 AA
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32.8%;
                          Best Local Similarity 50.7%;
Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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US-09-297-092-1.rspt

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Query Match
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                     Matches
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                                                                                                                                                                                                                                                                                                          12;
                                                                                                                              CSRKPLHVNFKELGWDDWIIAPLDYEAYHCEGLCDFPLRSHLEPTNHAIIQTLMNSMDPE 219
                                                                                                                                                                                                                                                                                                                                                                                                                      100 REIREKIRAMKSRKFSNPTPEHSIKGHPRHRRRRTALAGRPGVGPITSGGKGGGRRRTR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lytechinus variegatus (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae; Lytechinus.
                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Actinopterygii,
Neopterygii, Teleostei, Euteleostei, Ostariophysi, Cypriniformes,
Cyprinoidea, Cyprinidae, Rasborinae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A BMP pathway regulates cell fate allocation along the sea urchin animal-vegetal embryonic axis.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
EMBL; AF119712; AAD28038.1; ...
                                                                                                                                                                                                                                                                                                                                                                                40 KQHRTAEDTRLLCLSISAVSDSNNEAVHPGMLGLSREDQQTHERALLVAFSQARRKENLF
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                                                                                                                                                                                                                                                                                      Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
ANGERER L.M., OLEKSYN D.W., LOGAN C.Y., MCCLAY D.R., DALE
ANGERER R.C.;
                                                                                                                                                                                                                                                                                                       Indels
                                                  annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STPPSCCVPSKLSPISILYIDSGNNVVYKQYEDMVVESCGCR 261
                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update
                                                                                                                                                                                                                                                                                    22.2%; Score 813; DB 13; I
larity 55.9%; Pred. No. 1.19e-138;
Conservative 41; Mismatches 39;
                                                                                                                                                                                                                                                                 SEQUENCE 261 AA; 29414 MW; 82E59637 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417 AA; 47727 MW; AE44D1A9 CRC32;
                                                                                 Brachydanio rerio (Zebrafish) (Zebra danio).
          261 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 AA.
                                                 01-NOV-1999 (TrEMBLrel. 12, Last annotation GROWTH/DIFFERENTIATION FACTOR 7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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01.NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
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                                                                                                                                                                                                                                                                                             Local Similarity
les 124; Conser
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SEQUENCE 4
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7 7
09W6C0
                  09W6C0;
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                                                                                                                                                                                128 TEHHRHTVIFNISTMPAEEVLTMAELRLFRKDLEEHSIAKRHALDDRKSLEPIHYMQRIN 187
                                                                                                                                                                                                                                                                                                                                                               247 -SRGRPSPNHHHVRVTREADPSKVQELQ-NEEDERWFQTRPQIVTY-SDDGRTKRSP-SS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 RTKRSTSSSRSRKRKGKRLKANCRRHPLYVDFSDVHWNDWIVAPAGYQAYYCHGECPFPL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 AEHLNTTNHAIVOTLVNSVNPALVPKACCVPTELSAISMLYLDEYEKVVLKNYODMVVEG 200
                                                                                         68 KERPRPQGKLRVPQYMMDLYRSHTEHQDGISMHFDFDHLSTGTANTIRSYHHEDAGQVLP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Echinodermata; Echinozoa; Echinoidea;
Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae; Tripneustes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HWANG S.-P.L., CHEN C.A., CHEN C.-P.;
"Sea urchin TgBME2/4 gene encoding a bone morphogenetic protein
"closely related to vertebrate BMP2 and BMP4 with maximal expression
the later stages of embryonic development.";
Biochem. Biochem. Brophys. Res. Commun. 258:457-463(1999).
-I. SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
EMBL, AFI33305; AAD30538.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                     270 SGRQPASLLDVR-SVPGLDGSGW-EVFDI-WKLFRNFKNSAQLCLELEAWERGRAVDLRG
                                                                                                                                                                                                                                                                                                                                                                                        188 VFHILKPVARNRDTIKRLIDTRLVDVRNSSWESF-DVRPAVTSWVEVPEKNHGLEIELID
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGRKRKGKRLKANCRRHPLYVDFSDVHWNDWIVAPAGYQAYYCHGECPFPLAEHLNTTNH
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                                             17;
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Pred. No. 3.98e-84;
27; Mismatches 31; Indels
  Length 417;
                                             82; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2/4 HOMOLOG (FRAGMENT).
                      Pred. No. 9.62e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 AA; 23697 MW; A0988AC4 CRC32;
  DB 5;
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    Score 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF133305; AAD30538.1; -. PROSITE; PS00250; TGF_BETA; 1.
16.0%;
llarity 32.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 15.1%;
Best Local Similarity 53.2%;
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                      Local Similarity
nes 114; Conser
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NON_TER
SEQUENCE 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 9
Q9XZ69
Q9XZ69;
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7 10 Q26468 Q26468;

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64 RKPT-PSKSA-VVPQ-YMLDLYYMHSENDDPNIRRPRSTMGKHVERAASRANTIRSFHHE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-FW;
MEDLINE; 98072322.
MEDLINE; 98072322.
KISHIMOTO Y., LEE K.H., ZON L., HAMMERSCHMIDT M., SCHULTE-MERKER S.;
"The molecular nature of zebrafish swirl: BMP2 function is essential during early dorsoventral patterning.";
Development 124:4457-4466(1997).
                                                                                  SAJI T., UENO N.; signaling in zebrafish mesoderm patterning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 RPALAPS-KEPLTRLLDTRLVQDSHTR-WESFDVGSAVARWARESQHNHGLLVEVL-HPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 ESEVSEEAESNRRKHVRVSRSLHADEDSWAQARPLLVT-Y-SHDGQG-TAV---LHSNRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 KRQARRGQKP-RR-KHHQRSNCRRHALYVDFSDVGWNEWIVAPPGYHAFYCHGECPFPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 DHLNSTNHAIVQTLVNSVNSN-IPKACCIPTELSPISLLYLDEYEKVILKNYQDMVVEGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEE K.H., MARDEN J.J., THOMPSON M.S., MACLENNAN H., KISHIMOTO Y., PRATT S.J., SCHULTE-MERKER S., HAMMERSCHMIDT M., JOHNSON S.L., POSTLETHWAITE J.H., BEIER D.C., ZON L.I.;

"Cloning and Genetic Mapping of Zebrafish BMP-2.";

Dev. Genet. 23:0-0(1998).

"S.J., ARC25595.1;

HSSP; P18075; 1BMP.

PROSITE: PSO0250; TGF.BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 551; DB 13; Length 411;
Pred. No. 1.03e-83;
98; Mismatches 116; Indels 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMPHIBMP2/4.
Branchiostoma floridae (Florida lancelet) (Amphioxus).
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2/4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  411 AA; 46873 MW; AF0342A5 CRC32;
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PFAM; PF00688; TGFD_propeptide; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.0%;
llarity 32.2%;
Conservative
                                                 MEDLINE: 97231284.
NIKAIDO M., TADA M., SAJI 7
"Conservation of BMP signal
Mech. Dev. 61:75-88(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY:
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nes 117; Conserv
                                                                                                                                                                                                    SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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SEQUENCE 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 PFPLSAHMNSTNHAVVQTLMNSMNPGLVPKACCIPTQLTSISMLYLDEESKVVLKNYHEM 183
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  М.Д.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          NEWFELD S.J., GELBART W.M.; "Identification of two Drosophila TGF-beta family members in the grasshopper Schistocerca americana."; J. Mol. Bvol. 41:155-160(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PADGETT R.W., JOHNSTON R.D., GELBART W.M.; "A transcript from a Drosophila pattern gene predicts a protein homologous to the transforming growth factor-beta family."; Nature 325:81-84(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 242:1528-1534(1988).
-1- SINILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY:
EMBL; U23785; AAR81169.1; -.
HSSP; P18075; 1BMP.
                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
11-NOV-1999 (TrEMBLRel. 12, Last annotation update)
Schistocerca americana (American grasshopper).
Schistocerca americana (American grasshopper).
Bukaryota, Metazoa, Arthropoda, Tracheatta, Hexapoda, Insecta, Pterygota; Neoptera; Orthopteroidea; Orthopteroidea; Orthopteroidea; Acridomorpha; Acridoidea; Acrididae; Cyrtacanthacridinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WOZNEY J.M., ROSEN V., CELESTE A.J., MITSOCK L.M., WHITTERS KRIZ R.W., HEWICK R.M., WANG E.A.; "Novel regulators of bone formation: molecular clones and activities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Mismatches 27; Indels
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 551; DB 5;
Pred. No. 1.03e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 AA; 21879 MW; ED3D3318 CRC32;
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                           191
                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00019; TGF-beta; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64; Conservative
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                        PRELÌMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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093369;
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PROSITE;

99 Matches

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RNKSSSHQES-SRMPSV-GDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYAAFYCD 382
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                                                                                                                                                                    Created)
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PFAM; PF00019; TGF-beta; 1.
PFAM; PF00688; TGFb_propeptide; 1.
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Local Similarity 31.7%;
hes 115; Conservative 1
                                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                               BONE MORPHOGENETIC PROTEIN. ZBMP-2.
                                                                                                                                               PRELIMINARY;
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TISSUE=WHOLE EMBRYO;
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                                                                                                      491 EDMVVESCGCR 501
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GCR 501
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Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                212 IQIS-IYQI-IKEYPN-RDADLFLLDTRKAQASD-VGWFVFDITVTSNHWVINPQNNLGL 267
                                                                                                                                                                                                                     KKORRELKANCRRHSLYVDFSDVGWNDWIVAPPGYQAYYCHGECPFPLADHLNSTNHAIV 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 QLCAETGDGRSINVKSAGL-IGRHGPQSKQPFMV-AFFKASEVLFRSVRA-ANNKRKNQN 324
                                                                                                                                                                                                  Gaps
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X MEDILINE; 97000882.

T "Differential expression of bone morphogenetic proteins in the developing vestibular and auditory sensory organs.";

J. Neurosci. 16:6463-6475(1996).

J. Neurosci. 16:6463-6475(1996).

HEND: 883278; AAA49514.1;

R PRAM; PF00195; TGF_BETA; 1.

R PRAM; PF00109; TGF_DETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 PGGGRAAQLKLSSCPSGRQPA-SLLDVRSVPGLDGSGWEVFDIWKLFRNF-KNS-AQLCL
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
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                                                                                                                                                                                                                                                              310 QTLVNSVNPLAVPKACCVPTDLSPISMLYLNENDQVVLKNYQDMVVEGCGCR 361
                                                                                                                                                                                                                                                                         Length 453;
                                                                                                                                                                             Length 361;
                                                                                                                                                                  Score 546; DB 5; Length Jol. Pred. No. 1.10e-82;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   453 AA; 51628 MW; 72F385A0 CRC32;
                                                                                                                                                        361 AA; 41517 MW; 3C5F7E25 CRC32;
                                                                                                                                                                                                                                                                                                                              453 AA
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                                                                                                                                   PROSITE; PS00250; TGF_BETA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 30.5%;
Matches 95; Conservative
                                                                                                                                                                            Match 14.9%;
Local Similarity 55.4%;
es 62; Conservative
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                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
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                            SEQUENCE FROM N.A. MEDLINE; 98401944.
          Branchiostoma
                                                                                                                                              Glycoprotein.
SEQUENCE 36
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P87373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAFEALSSLKGKTTQQFFFNLTSIPGEELISAADVRIFRDQVLGDASTSGFHRINIYEVF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachydanio rerio (Zebrafish) (Zebra danio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Buteleostei; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE; 97231284.
MINAIDO M., TADA M., SAJI T., UENO N.;
"Conservation of BMP signaling in zebrafish mesoderm patterning.";
Mech. Dev. 61:75-88(1997).
-- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
EMBL; D49971; BAA24406.1;
-- HSSP; P18075; 1BMP.
321 AVDLRGLGFDRAARQVH-EKALFL-VFGRTKKRDLFFNEIKARSGQDDKTVYEYLFSQRR
                                                                 ESEVSEEAESNRRKHVRVSRSLHADEDSWAQARPLLVT-Y-SHDGQG-TAV---LHSNRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 KRQARRGQKP-RR-KHHQRSNCRRHALYVDFSDVGWNEWIVAPPGYHAFYCHGECPFPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 RPALAPS-KEPLTRLLDTRLVQDSHTR-WESFDVGSAVARWARESQHNHGLLVEVL-HPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 543; DB 13; Length 411;
Pred. No. 4.58e-82;
100; Mismatches 116; Indels 32;
                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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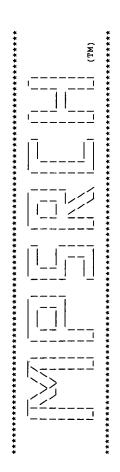
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Search completed: Wed Apr 19 19:48:43 2000 $J_{\overline{Q}D}$ time : 270 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp Run on:

Wed Apr 19 19:41:59 2000; MasPar time 36.54 Seconds 409.433 Million cell updates/sec lar output not generated.

>US-09-297-092-1 (1-501) from US09297092.pep 3662 Title:

1 MRLPKLLTFLLWYLAWLDLE......ANNVYKQYEDMVVESCGCR 501 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

82229 segs, 29864866 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot38 1:swissprot Database:

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 50.721; Variance 91.436; scale 0.555

SUMMARIES

		æ					
Result	Score	Query Match	Ouery Match Length	DB	ID	Description	Pred. No.
	3608	98.5	501	7	GDF5_HUMAN	GROWTH/DIFFERENTIATION	0.00e+00
7	3332	91.0		-	GDF5_MOUSE	GROWTH/DIFFERENTIATION	0.00e+00
m	939	25.6	436	-	GDF6_BOVIN	GROWTH/DIFFERENTIATION	1.63e-176
4	832	22.7		-	GDF6_MOUSE	GROWTH/DIFFERENTIATION	3.69e-152
υ.	735	20.1	151	~	GDF7_MOUSE	GROWTH/DIFFERENTIATION	3.01e-130
9	995	15.5	405	-	BMP4_CHICK	BONE MORPHOGENETIC PRO	1.32e-92
7	565	15.4	396	Н	BMP2_DAMDA	BONE MORPHOGENETIC PRO	2.20e-92
89	544	14.9	393	Н	BMP2_RAT	BONE MORPHOGENETIC PRO	9.04e-88
6	544	14.9	395	-	BMP2_RABIT	BONE MORPHOGENETIC PRO	9.04e-88
10	546	14.9	396	-	BMP2_HUMAN	BONE MORPHOGENETIC PRO	3.29e-88
11	545	14.9	398	-	BMPA_XENLA	BONE MORPHOGENETIC PRO	5.46e-88
12	546	14.9	452	Н	BMP5_MOUSE	BONE MORPHOGENETIC PRO	3.29e-88
13	543	14.8	454	~	BMP5_HUMAN	BONE MORPHOGENETIC PRO	1.50e-87
14	533	14.6	394	-	BMP2_MOUSE	BONE MORPHOGENETIC PRO	2.33e-85
15	536	14.6	398	Н	BMPB_XENLA	BONE MORPHOGENETIC PRO	5.12e-86
16	533	14.6	408	-	BMP4_HUMAN	BONE MORPHOGENETIC PRO	2.33e-85
17	531	14.5	372	Н	DECA_TRICA	DECAPENTAPLEGIC PROTEI	6.37e-85
18	532	14.5	408	-	BMP4_DAMDA	BONE MORPHOGENETIC PRO	3.85e-85
19	530	14.5	408	-	BMP4_MOUSE	BONE MORPHOGENETIC PRO	1.05e-84
20	530	14.5	408	Н	BMP4_RAT	BONE MORPHOGENETIC PRO	1.05e-84
21	529	14.4	401	-	BMP4_XENLA	BONE MORPHOGENETIC PRO	1.74e-84
22	529	14.4	409	-	BMP4_RABIT	BONE MORPHOGENETIC PRO	1.74e-84
23	523	14.3	383	-	UNIV_STRPU	UNIVIN PRECURSOR.	3.57e-83

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5.91e-83	1.31e-83	1.31e-83	1.99e-81	7.30e-82	8.99e-81	4.05e-80	3.68e-78	1.00e-77	3.32e-76	3.32e-76	9.02e-76	3.32e-76	1.49e-75	1.49e-75	1.49e-75	7.10e-72	1.92e-71	2.75e-69	1.04e - 63	1.04e-63	1.01e-60
BONE MORPHOGENETIC PRO	DECAPENTAPLEGIC PROTEI	DECAPENTAPLEGIC PROTEI	BONE MORPHOGENETIC PRO	DVR-1 PROTEIN HOMOLOG	BONE MORPHOGENETIC PRO	BONE MORPHOGENETIC PRO	DECAPENTAPLEGIC PROTEI	BONE MORPHOGENETIC PRO	BONE MORPHOGENETIC PRO	DVR-1 PROTEIN PRECURSO	BONE MORPHOGENETIC PRO	BONE MORPHOGENETIC PRO	BONE MORPHOGENETIC PRO	60A PROTEIN PRECURSOR	BONE MORPHOGENETIC PRO	DORSALIN-1 PRECURSOR (DVR-1 PROTEIN PRECURSO	60A PROTEIN PRECURSOR	BONE MORPHOGENETIC PRO	BONE MORPHOGENETIC PRO	BONE MORPHOGENETIC PRO
BM8A_MOUSE	DECA_DROME	DECA_DROSI	BMP2_CHICK	DVR1_STRPU	BMP7_HUMAN	BMP7_MOUSE	DECA_DROPS	BMP8_HUMAN	BMP6_RAT	DVR1_BRARE	BMP7_XENLA	BMP6_HUMAN	BM8B_MOUSE	60A_DROVI	BMP6_MOUSE	DSL1_CHICK	DVR1_XENLA	60A_DROME	BMP3_RAT	BMP3_HUMAN	BM3B_RAT
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399	588	593	353	461	431	430	621	402	207	355	426	513	399	436	510	427	360	455	468	472	476
14.3	14.3	14.3	14.1	14.1	14.0	13.9	13.7	13.6	13.4	13.4	13.4	13.4	13.3	13.3	13.3	12.9	12.8	12.5	11.8	11.8	11.4
522	525	525	515	517	512	209	200	498	491	491	489	491	488	488	488	471	469	459	433	433	419
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AA. .e.) late) ! (GDF-5) (CARTILAGE-DERIVED	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1] SEQUENCE FROM N.A. TISSUE-PIACENTA; MEDLINE; 95071375. MEDLINE; 95071375. "Cloning and expression of recombinant human growth/differentiation factor 5."; Biochem. Biophys. Res. Commun. 204:646-652(1994). SEQUENCE FROM N.A. TISSUE-ARTICIARR CARTILAGE; TISSUE-ARTILAGE;	CHANG S., HOANG B., THOMAS J.T., VUXICEVIC S., LUYTEN F.P., RYBA N.J.P., KOZAK C.A., REDDI A.H., MOOS M.; "Cartilage-derived morphogenetic proteins. New members of the "Cartilage-derived morphogenetic proteins. New members of the transforming growth factor-beta superfamily predominantly expressed in long bones during human embryonic development."; J. Biol. Chem. 269:28227-28234(1994)!- FUNCTION: COULD BE INVOLVED IN BONE FORMATION!- FUNCTION: COULD BE INVOLVED IN BONE FORMATION!- SUBGNUTT: HOMODIMER, DISULETIDE-LINKED (BY SIMILARITY).	HUMAN EMBRYONIC DEVELOPMENT. -!- DISEASE: DEFECTS IN GDF5 ARE A CAUSE OF ACROMESOMELIC CHONDRODYSPLASIA OF THE HUNTER-THOMPSON TYPE. THIS FORM OF DWARFISM IS CHARACTERIZED BY SHORT FOREARMS, HANDS AND FEET. THE RADIUS IS CURVED AND ITS HEAD IS OFTEN DISLOCATED POSTERIORLY. IT METACARPALS, METATARASIS AND PHALANGES ARE PARTICULARLY SHORT. THE PHALANGES ARE ALMOST SQUARE!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.	This SWISS-PROT entry is copyright. It is produced through a collabor between the Swiss Institute of Bioinformatics and the EMBL outstat the European moinformatics Institute. There are no restrictions or use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for comme
501 updat n upd URSOR	ta; V nidae B., nt hu	ICEVI MOOS teins rfami deve ONE F	AUSE HOMPS RT FO OFTE LANGE	It is nform e. T long emove
NUDARD; PRT; 501 AA. 32, Created) 33, Last sequence update) 35, Last annotation update) NTION FACTOR 5 PRECURSOR (GD	Chordata; Craniata; Vertebra Catarrhini; Hominidae; Homo. TH., JACOBOWSKY B., POHL J.;ion of recombinant human gross. Commun. 204:646-652(1994)	J.T., VUK SDDI A.H., enetic pro beta supe embryonic 3234(1994) DIVED IN B SULFIDE-LI	HUMAN EMBRYONIC DEVELOPMENT. DISEASE: DEFECTS IN GDF5 ARE A CAUSE OF ACR CHONDRODYSPLASIA OF THE HUNTER-THOMESON TYP DWARFISM IS CHARACTERIZED BY SHORT FOREARMS RADIUS IS CURVED AND ITS HEAD IS OFTEN DISL PHALANGES ARE PHALANGES ARE ALMOST SQUARE. SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.	SS-PROT entry is copyright. It is the Swiss Institute of Bioinforma pean Bioinformatics Institute. Th non-profit institutions as long and this statement is not removed
STANDARD; 1. 32, Creat 1. 33, Last 1. 35, Last 1. 35, Last TIATION FACT ROTEIN 1) (C	; Chordat; Catarrh; Catarrh RDT H., Ssion of Res. Comm	C.A., RE morphoge h factor-ng human:28227-28 D BE INVCIMER, DIE CITY: PRE	HUMAN EMBRYONIC DEVELOPMENT. DISEASE: DEFECTS IN GDF5 ARE CHONDRODYSPLASIA OF THE HUNT DWARFISM IS CHARACTERIZED BY RADIUG IS CUNYED AND ITS HEA METACARPALS, METATARSALS AND PHALANGES ARE ALMOST SQUARE. SIMILARITY: BELONGS TO THE T	try is cc Institut formatics t instit
STA (Rel. (Rel. (Rel. RENTIA C PROT	etazoa imates M N.A. NIA; NEIDHA expre phys. M N.A.	ANG B. KOZAK erived growt s duri n. 269 HOMOD	BRYONI DEFEC YSPLAS IS CH S CURV ALS, M	ROT en Swiss Bioin -profi
T 1 GDE5_HUMAN STANDARD; PRT; 501 AA. P43026; 01-NOV-1995 (Rel. 32, Created) 01-FEBER 1996 (Rel. 33, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) GROWTH/DIFFERRITIATION FACTOR 5 PRECURSOR (GDF-5) MORPHOGENETIC PROTEIN 1) (CDMP-1). Homo sapiens (Human).	EUKATYOCA: MCTAZOA; Chordat EUTHERIA: PTIMATES; CATAITH [1] SEQUENCE FROM N.A. SEGUENCE FROM N.A. MEDLINE; 95071375. MCDLINE; 95071375. MCDLINE; 95071375. MCDLINE; 95071375. MCDLINE; 95071375. MCDLINE; 95071375. MCDLINE; 9507114068; MCDLINE; 950751014408; MCDLINE; 950751014408;	CHANG S., HOANG B., THOMAS J.T., VUKICEVIC S., LUYT RYBA N.J.P., KOZAK C.A., REDDI A.H., MOOS M.; CATLILAGE-derived morphogenetic proteins. New memb transforming growth factor-beta superfamily predomin in long bones during human embryonic development."; J. Biol. Chem. 269:28727-28234(1994)!- FUNCTION: COULD BE INVOLVED IN BONE FORMATION!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILA.)!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN	HUMAN EMI -!- DISEASE: CHONDRODY DWARFISM RADIUS IS METACARP? PHALANGE: -!- SIMILARI	This SWISS-Properties the European use by non-modified and
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Pred. No. 0.00e+00;
4; Mismatches 4; Indels (
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I -> A (IN REF. 1).
S -> L (IN REF. 1).
712C0300 CRC32;
        or send an email to license@isb-sib.ch)
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                                                                   PROSITE; PS00250; TGF_BETA; 1. PFAM; PF00019; TGF-beta; 1. PFAM; PF00688; TGFD_propeptide
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GDF5_MOUSE STANDARD; 1
P43027;
01-NOV-1995 (Rel. 32, Created)
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                     EMBL; X80915; CAA56874.1; -. EMBL; U13660; AAA57007.1; -. HSSP; P18075; 1BMP.
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493; Conservative
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                                            MIM; 601146; -. MIM; 201250; -. MIM; 200700; -.
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SIGNAL
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                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                      "Limb alterations in brachypodism mice due to mutations in a member of the TGF beta-superfamily.";
Nature 368:639-643(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ŋ.
                                                                                                                                                                                                                                                                                                                                                                          -i- SUBUNIT: HOWODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-i- DISEASE: DEFECTS IN GDF-5 ARE THE CAUSE OF BRACHYPODISM ALTERS THE LENGTH AND NUMBERS OF BONES IN THE LIMBS BUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00019; TGF-beta: 1.
PFAM; PF00689; TGF-beta: 1.
Signal; Growth factor; Cytokine; Glycoprotein; Polymorphism.
SIGNAL 1 ? POTENTIAL.
PROPEP ? 375 POTENTIAL.
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BY SIMILARITY.
BY SIMILARITY.
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Pred. No. 0.00e+00;
23; Mismatches 15; Indels
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POTENTIAL.
S -> P.
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 5 PRECURSOR (GDF-5)
                                                                                                                                                                                                                                                                                                                                                        -! - FUNCTION: COULD BE INVOLVED IN BONE FORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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PROSITE; PS00250; TGF_BETA; 1.
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                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CD-1; TISSUE-EMBRYO;
MEDLINE; 94195427.
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1 Similarity 91.2%;
457; Conservative
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4460
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183
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                                                                   GDF5 OR GDF-5 OR BP
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or send an email to license@isb-sib.ch).
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               RSGQDDKTVYEYLFSQRRKRRAPLANRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIA 414
                                                                                                                   PLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID 474
RNFKNSAQLCLELEAWERGRAVDLRGLGFERTARQVHEKALFLVFGRTKKRDLFFNEIKA 354
                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 6 PRECURSOR (GDF-6) (CARTILAGE-DERIVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUB-ARTICULAR CARTILAGE;
MEDILINE; 95050604.
CHANG S., HOANG B., THOMAS J.T., VUKICEVIC S., LUYTEN F.P.,
RYBA N.J.P., KOZAK C.A., REDDI A.H., MOOS M.;
"Cartilage-derived morphogenetic proteins. New members of the transforming growth factor-beta superfamily predominantly expressed
                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
Bovinae; Bos.
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GROWTH/DIFFERENTIATION FACTOR 6.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
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Pred. No. 1.63e-176;
85; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in long bonés during human embryonic development.";
-1. Biol. Chem. 269:28227(2944).
-1. SUBGNIT: HOWODIMER, DISGLFIDE-LINKED (BY SIMILARITY).
-1. SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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                                                                                                                                                                                                                                                                        436 AA.
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PROSITE; PS00250; TGF_BETA; 1.
PFAM; PF00019; TGF-beta; 1.
PFAM; PF00688; TGFb_propeptide; 1.
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llarity 47.6%;
Conservative
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P55106;
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RRPPQQPEAREPPGRGPRLVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDR 108

49

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Matches

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                                                                                   219
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150 REPGPPREPKEP-FRPPPITPHEYMLSLYRTLSDADRKGGNSSVKLEAGLANTITSFIDK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STORM E.E., HUYNH T.V., COPELAND N.G., JENKINS N.A., KINGSLEY D.M., LEE S.-J.;
                            GLDDLSHTPLRRQKYLFDVSTLSDKEELVGADVRLFRQAPAALA-P--PAAAPLAALRLP
                                           166 VAPAA---GSA-E-PGPAGAPRPGWEVFDVWRGLRP-QPWKQLCLELRAAWGGEPGAAED
                                                                                                EARTPGPQOPPPDLRSLGFGRRVRTPQERALLVVFSRSQRKTLFAEMREQLGSATEVVG
                                                                                                                                                       280 PGGGAEGSGPPPPPPPPPPSGTPDAGLWSPSPGRRRRTAFASRHGKRHGKKSRLRCSKKP
                                                                                                                                                                                                              340 LHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPS
                                                                                                                                                                                                                                                                  "Limb alterations in brachypodism mice due to mutations in a new member of the TGF beta-superfamily.";
Mature 368:639-643(1994).
-i- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 6 PRECURSOR (GDF-6) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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GROWTH/DIFFERENTIATION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

INTERCHAIN (BY SIM

'; AEE04314 CRC32;
                                                                                                                                                                                                                                                                                                          CCVPTKLTPISILYIDAGNNVVYNEYEEMVVESCGCR 436
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                                                                                                                                                                                                                                                                                                                                                                                              125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:95689; GDF6.
PROSTIE: PSOOZSO; TGE_BETA; 1.
PRAM: PF00019; TGF-beta; 1.
Growth factor; Cytokine; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 GF
90 BN
122 BN
124 BN
89 IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-LIVER;
MEDLINE; 94195427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U08338; AAA18779.1; -.
                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 1 24 53 1 57 1 125 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P18075; 1BMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDF6 OR GDF-6.
                                                                                                                                                                                                                                                                                                                                                                                         GDF6_MOUSE
P43028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
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CARBOHYD
CARBOHYD
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                                                    LRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVTKQYEDMVVE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRGHGRRGRSRCSRKSLHVDFKELGWDDWIIAPLDYEAYHCEGVCDFPLRSHLEPTNHAI 98
                                          1 RRRRRTAFASRHGKRHGKKSRLRCSRKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFP 60
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                        MEDLINE; 94195427.
STORM E.E., HUYNH T.V., COPELAND N.G., JENKINS N.A., KINGSLEY D.M.,
                                                                                                                                                                                                                                                                                                                                            LEE S.-J.;
"Limb atterations in brachypodism mice due to mutations in a new member of the TGF beta-superfamily.";
Nature 368:639-643(1994).
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                                                                                                                                                                           RESULT 5
GDF-Z-MOUSE STANDARD; PRT; 151 AA.

GDF-Z-MOUSE STANDARD; PRT; 151 AA.

D1 NOV-1995 (Rel. 32, Created)
D2 01-NOV-1997 (Rel. 35, Last aequence update)
DF 01-NOV-1997 (Rel. 35, Last annotation update)
DF GROWTH/DIFFERENTIATION FACTOR 7 PRECURSOR (GDF-7) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GROWTH/DIFFERENTIATION FACTOR 7.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
POLY-ARG.
                                                                                                                                                                                                                                                                         Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 151;
Length 125;
                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
Score 832; DB 1; L
Pred. No. 3.69e-152;
22; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 735; DB 1; L
Pred. No. 3.01e-130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62377F04 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:95690; GDF7.
PROSITE; PS00250; TGF_BETA; 1.
PFAM; PF00019; TGF-beta; 1.
GTowth factor; Cytokine; Glycoprotein.
NON TER 1 1 1 1 1 PROPEP <1 5 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15697 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U08339; AAA18780.1; -.
                                                                                                                                                                                                                                                                                                              STRAIN-BALB/C; TISSUE-LIVER; MEDLINE; 94195427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.1%;
           79.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        larity 74.3%;
Conservative
                      99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
116
148
150
115
                                                                                                                                                                                                                                                              musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 AA;
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                          SCGCR 125
                                                                                                                                       SCGCR 501
                                                                                                                                                                                                                                                    OR GDF-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
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Matches
                                                                                                                                             497
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                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 HPPQTRQATARTVTP-KGQLPGGKAPPKAGSVPSSFLLKKAREPGPPREPKEPFRPPPIT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-SYMLDLYRLQSGEEEERSLQEISLQYPERSASRANTVRSFHHEEHLESVPGPSEAPRI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFVFNLSSVPDNEVISSEELRLYREQVEEPSAAWERGFHRINIYEVMKPLSERSQAITRL 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, X75915; CANCELLERD, 1.
HSSP, P18075; 1BMP.
HSSP, PROSTIE; PS00250; TGF_BETA; 1.
PFAM; PF00019; TGF-Deta; 1.
PFAM; PF00688; TGFD_Propeptide; 1.
PFAM; PF00688; TGFD_PROPERING; TGFD_PRO
Pred. No. 1.32e-92;
89; Mismatches 152; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
A60C5A50 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 566; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY S
                                                                                                                                                                                                                    405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ξ.
MM
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llarity 32.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46057
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=
::
                                                                                                                                                                                                                                                                                                                                                                                                                                 BMP4 OR BMP-4.
Gallus gallus (Chicken).
                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291
405
370
402
404
369
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208
347
362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 130; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200
292
395
334
338
369
144
347
405 AA;
                                                                                                                                                                           LT 6
BMP4_CHICK
Q90752;
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313 417

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                                                                                                                                                                                                                     94 APGHRLERAASLANTVRTFHHEESLEELPEMSGKTTRRFFFNLTSIPTEEFITSAELQVF 153
                                                                                                                                                      314 IVAPPGYHAFYCHGECPFPLADHLNSTNHAIVQTLVNSVNSK-IPKACCVPTELSAISML 372
                                                                                                                                                                                                                                                                                                                                                   S.E.;
     PGRSSSQPSDDVLSEFELRLLSMFGLKQRPT-PSRDP-VVPP-YMLDLYR-LHSGQPGAP
                                                                                   GKHMPEALENNSSFHHRINIFEIIKPATANSKFPVTRLLDTRLVTQ-NASRWESFDV-TP
                                                                                                                                                                                                                                                                 V-T-FGHDGKG-HP-L--HRREKR-Q-A-KH-KQR-KRLKSSCKRHPLYVDFSDVGWNDW
                                                                                                                                                                                                                                                                                      :: |:| | :| |: || :|| |: || 358 IKARSGQDDKTVYEYLFSQRRKRAPLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDW
                                                                                                                                                                                                  -AVMRWTAQG-LTNHGFV-V-EVAHPEDSYGASKRHVRISRSLHQDEHSWSQIRPLL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE: PSO(25): TGF BETA; 1.
PROSITE: PSO(015): TGF-beta; 1.
PFAM; PF00689; TGFD_propeptide; 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (BMP-2A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN (BY SIMILARITY).
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BONE MORPHOGENETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                               373 YLDENEKVVLKNYQDMVVEGCGCR 396
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z25868; CAA81088.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279
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133
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1133
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BMP2_RAT
P49001;
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DISULFID
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31;
                              254 I-SRSLPQGHGGDWAQL-RPLLVTFGHDGRG-HA-L-T-RRARRSP--KHHGSR--KN-K 302
                                                                                               303 KNCRRHALYVDFSDVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNSTNHAIVQTLVNSVN 362
LDVRSVPGLDGSGWEVFDIWKLFRNFKNSAQLCLELEAWERGRAVDLRGLGFDRAARQVH 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Bone morphogenetic protein 2 transcripts in rapidly developing deer antler tissue contain an extended 5' non-coding region arising from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Cetartiodactyla, Ruminantia, Pecora, Cervoidea, Cervidae,
                                                    EMBL, AJ001817; CAA05033.1; -.
HSSP; P18075; 1BMP.
PROSITE; PS00250; TGF_BBTA; 1.
PFAM; PF00019; TGF-beta; 1.
PFAM; PF00688; TGPD_propeptide; 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FENG J.Q., CHEN D., GHOSH-CHOUDHURY N., ESPARZA J., MUNDY G.R.,
HARRIS S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 565; DB 1; Length 396;
Pred. No. 2.20e-92;
97; Mismatches 127; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BONE MORPHOGENETIC PROTEIN 2
BY SIMILARITY.
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INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                S-SIPKACCVPTELSAISMLYLDEYDKVVLKNYQEMVVEGCGCR 405
                                                                                                                                                                               : | | :||||| ||:||:||:|| | ::|| | | ::|||||:||||| 458 PESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          distal promoter.";
Biochim. Biophys. Acta 1350:47-52(1997).
-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
-!- SUBUNIT: HOWODIMER, DISULFIDE-LINKED.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8C56358B CRC32;
                                                                                                                                                                                                                                                               396 AA
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32.3%;
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Matches 124; Conservative
                                                                                                                                                                                                                                                                 STANDARD;
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396 AA;
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SEQUENCE FROM N.A.
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MEDLINE; 97157076.
                                                                                                                                                                                                                                                                                                                                                                                                                            Cervinae; Cervus.
                                                                                                                                                                                                                                                            BMP2_DAMDA
O19006;
15-JUL-1998
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BMP2.

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                                                               Gaps 26;
                                                                                                                                                                          245
                                                                                                                                                                                                                               340 ALFL-VFGRTKKRDLFFNEJKARSGODDKTVYEYLFSQRRKRRAPLATRQGKRPSKNLKA 398
                                                                                     72 VVPP-YMLDLYRRHSGQPGALAPDHRLERAASRANTVLSFHHEEAIEELSEMSGKTSRRF 130
                                                                                                 131 FFNLSSVPTDEFLTSAELQIFREQMQEALGNSSFQHRINIYEIIKPATASSKFPVTRLLD 190
                                                                                                                                                                                                                                                            SCKRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNSTNHAIVQTLVNSVNS 351
                                                                                                                                                                                                                                                                                  399 RCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDP 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 TRLVTQ-NTSQWESFDVTPAVMRWTAQGHTNHGFVV-EVAHLEEKPGVS-KRHVR-I-SR
                                                                                                                                                                                                                    SLHQDEHSWSQVRPLL---V-T-FGHDGKG-HP-L--HKREKR-Q-A-KH-KQR-KRLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STATE, TISSUE-CCULAR CILLARY EPITHELIUM; STRAIN-NEW SEALAND WHITE; TISSUE-CCULAR CILLARY EPITHELIUM; WAN X.L., SEARS J., CHEN S., SEARS M.; "Cloning and expression of BMP-2/-4 from rabbit ocular cillary
                                                               29;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                          Length 393;
                                         Score 544; DB 1; Length 393
Pred. No. 9.04e-88;
88; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                       K-IPKACCVPTELSAISMLYLDENEKVVLKNYQDMVVEGCGCR 393
                                                                                                                                                                                                                                                                                                                            501
                                                                                                                                                                                                                                                                                                                  459 ESTPPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGCR
                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2)
                      582689AF CRC32;
                                                                                                                                                                                                                                                                                                                                                                     395 AA
            POTENTIAL.
 POTENTIAL
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                     44383 MW;
                                          14.9%;
                                                    Best Local Similarity 32.7%;
Matches 112; Conservative
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 197
197 1
335 3
393 AA;
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BMP2_RABIT
046564;
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          CARBOHYD
                      SEQUENCE
                                           Query Match
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TISSUE SPECIFICITY: PARTICULARIX ABUNDANT IN LUNG, SPLEEN AND
COLON AND IN LOW BUT SIGNIFICANT LEVELS IN HEART, BRAIN, PLACENTA,
LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS, PROSTATE, OVARY AND
SMALL INTESTINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                     211
                                                                                                                                                                                                                                                                                                                                                                                           242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 PGGKAPPKAGS-VPSSFLLKKAREPGPPREPKEPFRPPPITPHEYMLSLYRTLS-DADRK 186
                                                                                                                                                                                                                                                                                                                                              93 APDHRLERAASRANTVRSFHHEESLEELPETSGKTTRRFFFNLTSIPPEEFITSAELQVF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 VMRWTAQGHANHGFVV-EVTHLEEKQGVS-KRHVR-I-SRSLHPDEHSWSQIRPLL---V 264
                                                                                                                                                                                                                                                    36 SSGRPSPQPSDDILSEFELRLLSMFGLKQRPT-PSRDA-VVPP-YMLDLYRRHSGQPGAP 92
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                        243 RKRPSDTAKPAAPGGGRAA--QLKLSSCPSGRQPAS-LLDVRSVPGLDGSGWEVFDIWKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REQMQEALGDDSGFHHRINIYEIIKPATANSKFPATRLLDTRLV-NQNTSRWESFDVTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265 -T-FGHDGKG-HP-L--HRREKR-Q-A-KH-KQR-KRLKSSCKRHPLYVDFSDVGWNDWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAPPGYHAFYCHGECPFPLADHLNSTNHAIVQTLVNSVNSK-IPKACCVPTELSAISMLY
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WOZNEY J.M., ROSEN V., CELESTE A.J., MITSOCK L.M., WHITTERS M.J., KRIZ R.W., HEWICK R.M., WANG E.A.;
"Novel regulators of bone formation: molecular clones and activities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCHEUFLER C., SEBALD W., HUELSMEYER M.; "Crystal structure of human bone morphogenetic protein-2 at 2.7
                                                                                                                                                                                                        33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                           Score 544; DB 1; Length 395;
                                                                                                                                                                                                        98; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (BMP-2A).
                       SIMILARITY).
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-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 292-396.
                                                                                                                                                                                Pred. No. 9.04e-88;
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                                                                                                                 81F38F1E CRC32;
                     INTERCHAIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396 AA.
  BY SIMILARITY
                                          POTENTIAL.
                                                                    POTENTIAL.
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                                                                                                                                                           14.9%;
                                                                                                                                                                                   Local Similarity 31.1%;
                                                                                                                                                                                                     119; Conservative
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                                                                                                            395 AA;
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328
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134
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                                                               CARBOHYD
CARBOHYD
DISULFID
                                            CARBOHYD
                                                                                                            SEQUENCE
                                                                                                                                                             Query Match
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Matches
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                               between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                   This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 VMRWTAQGHANHGFVV-EVAHLEEKQGVS-KRHVR-I-SRSLHQDEHSWSQIRPLL--V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 -T-FGHDGKG-HP-L--HKREKR-Q-A-KH-KQR-KRLKSSCKRHPLYVDFSDVGWNDWI
                                                                                                                                                                                                                                                                                                                        Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 546; DB 1; Length 396;
Pred. No. 3.29e-88;
100; Mismatches 131; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                     BONE MORPHOGENETIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-UUL-1993 (Rel. 26, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2-I PRECURSOR (BMP-2-I).
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182782C0 CRC32;
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PROSTIE; PS00226; TGF_BETA; 1.
PFAM: PF00019; TGF-Deta; 1.
PFAM: PF00688; TGFD_Dropeptide; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDENEKVVLKNYQDMVVEGCGCR 396
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                                                                                                                                                                     EMBL; M22489; AAA51834.1; -.
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llarity 31.1%;
Conservative 1
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HSSP; P18075; 1BMP.
MIM; 112261; -.
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164
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200
396 AA;
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P25703;
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                                                                                                                                                                                                                                                                                                              NISHIMATSU S., SUZUKI A., SHODA A., MURAKAMI K., UENO N.;
"Genes for bone morphogenetic proteins are differentially transcribed
in early amphibian embryos.";
Biochem. Biophys. Res. Commun. 186:1487-1495(1992).
-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
-!- SUBUNIT: BELONGS TO THE TGF-BETA FAMILY.
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Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSUVZZZ, TGF-beta; 1.
PFAM; PF00019; TGF-beta; 1.
PFAM; PF00688; TGFD_propeptide; 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
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BONE MORPHOGENETIC PROTEIN 2-I.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                              MEDLINE, 91274367.
PLESSOW S., KOESTER M., KNOECHEL W.;
"CDNA sequence of Xenopus laevis bone morphogenetic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 398;
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Local Similarity 32.7%; Pred. No. 5.46e-88;
nes 126; Conservative 88; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S -> P (IN REF. 2).
V -> L (IN REF. 2).
N -> T (IN REF. 2).
3; 6143F996 CRC32;
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PIR; J10687; J10687.
HSSP; P10775; JBMP.
PROSITE; PS00250; TGF_BETA; 1.
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398 AA;
                                                                                             SEQUENCE FROM N.A.
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                      Batrachia;
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SEQUENCE FROM N.A.
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                      416
                                                           PEEYLVR-VSLAGEAKETRKGYPASP-NGYAHRLHLPPRTPLTTQSPPLASLHDTNFLND 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 -ADMVMSFVNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDKGNHRFENE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSRB; P18075; IBMF.

HSRSTPE P800250; TGF_BETA; I.

PRAM; PF00019; TGF_DETA; I.

DR Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.

FT SIGNAL

FT CHAIN

FT CHAIN

FT DISULFID 381 417 BY SIMILARITY.

FT DISULFID 384 451 BY SIMILARITY.

FT DISULFID 384 550 POTENTIAL.

FT DISULFID 384 550 POTENTIAL.

FT DISULFID 385 750 POTENTIAL.

FT DISULFID 386 750 POTENTIAL.

FT DISULFID 387 750 POTENTIAL.

FT DISULFID 388 750 POTENTIAL.

FT DISULFID 389 POTENTIAL.
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PLLVTFSHDGKG-HA-L--HKRQKR-Q-A-RH-KQR-KRLKSSCRRHPLYVDFSDVGWND
                                             WIVAPPGYHAFYCHGECPFPLADHLNSTNHAIVQTLVNSVNTN-IPKACCVPTELSAISM
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                                                                                                                                                                                                                                                                                                                                                    alterations
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                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 452;
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 28.8%; Pred. No. 3.29e-88;
nes 107; Conservative 101; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                       KING J.A., MARKER P.C., SEUNG K.J., KINGSLEY D.M.; "BMP5 and the molecular, skeletal, and soft-tissue short ear mice.";
                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
101-FEB-1996 (Rel. 33, Last annotation update)
BONE MORPHOGENETIC PROTEIN 5 PRECURSOR (BMP-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                    452 AA
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                                                                                             LYLDENEKVVLKNYQDMVVEGCGCR 398
                                                                                                        14.98;
                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            MEDLINE; 95046894.
                                                                                                                                                                                                                                          BMP5 OR BMP-5.
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                                                                                                                                                      LT 12
BMP5_MOUSE
P49003;
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                      357
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                                                                                                                                                        RESULT
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                                                                                                                                                                                                                                                                                                                 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                              324
                                                                                                                                                                                                                                                           LEL-EAWERGRAVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKTV 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELESTE, A.J., IANNAZZI J.A., TAYLOR R.C., HEWICK R.M., ROSEN V., WANG E.A., WOZNEY J.M.;

"Identification of transforming growth factor beta family members present in bone-inductive protein purified from bovine bone.";

Proc. Natl. Acad. Sci. U.S.A. 87:9843-9847(1990).

-! FUNCTION: INNDUCES CARTILAGE AND BONE FORMATION.

-! SUBULT: HONDIMER, DISULFIDE-LINKED (BY SIMILARITY).

-! TISSUE SPECIFICITY: EXPRESSED IN THE LUNGS AND LIVER.

-! SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
LQLCAETGDGRSINVKSAGLV-GRHGPQSKQPFMV-AFFKASEVLLRSVRAASKRKNQNR
                                                                                   TIKIS-IYQI-IKEY-TNRDADLFLLDTRKTQALD-VGWLVFDITVTSNHWVINPQNNLG
                                                                                                                          381 DGECSFPLNAHMNATNHAIVQTLVHLMFPDHVPKPCCAPTKLNAISVLYFDDSSNVILKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cartilage; Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BONE MORPHOGENETIC PROTEIN 5
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
BONE MORPHOGENETIC PROTEIN 5 PRECURSOR (BMP-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             454 AA
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PFAM; PF00688; TGFb_propeptide; 1.
Signal; Growth factor; Cytokine; Bone; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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HSSP; P18075; 1BMP.
MIM; 112265; -
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M60314; AAA36736.1; -.
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211
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490 YEDMVVESCGCR 501
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BMPB_XENLA
P30884;
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                Gaps 18;
                                                                                                     154 ADMVMSFVNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDRSNNRFENET 213
                                                                                                                                                                                                                                                        QLCAETGDGRSINVKSAGL -- VGRQGPQSKQPFMV - AFFKASEVLLRSVRAANKRKNQNR 326
                                                                                                                                                                                                                     EL-EAWERGRAVDLRGLGFDRAARQV-HEKALFLVFGRTKKRDLFFNEIKARSGQDDKTV 369
                                                                                                                                                                                                                                            NKS-SSHQDSSR--MSSV-GDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYAAFYC 382
                                                                                                                                                                                                                                                                                        383 DGECSFPLNAHMNATNHAIVQTLVHLMFPDHVPKPCCAPTKLNAISVLYFDDSSNVILKK 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DICKINSON M.E., KOBRIN M.S., SILAN C.M., KINGSLEY D.M., JUSTICE M.J., MILLER D.A., CECI J.D., LOCK L.F., LEE A., BUCHBERG A.M., SIRACUSA L.D., LYONS K.M., DERXNCK R., HOGAN B.L.M., COPELAND N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure and sequence of mouse bone morphogenetic protein-2 gene (BMP-2): comparison of the structures and promoter regions of BMP-2 and BMP-4 genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seven members of the murine TGF-beta inkage to several morphogenetic mutant
                                                                                                                   214 IKIS-IYQI-IKEY-TNRDADLFLLDTRKAQALD-VGWLVFDITVTSNHWVINPQNNLGL
                                                                                                                                                                255 PGGGRAAQLKLSSCPSGRQPA-SLLDVRSVPGLDGSGWEVFDIWKLFRNF-KNS-AQLCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FENG J.C., HARRIS M.A., GHOSH-CHOUDHURY N., FENG M., MUNDY G.R., HARRIS S.E.;
                                                                               20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                        Length 454;
                                                                               88; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1991 (Rel. 18, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -I- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
-I- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
-I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                        Score 543; DB 1; Pred. No. 1.50e-87;
                                 E59AC82B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                             394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochim. Biophys. Acta 1218:221-224(1994).
             POTENTIAL.
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                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Chromosomal localization of seven
superfamily suggests close linkage
                                 51736 MW;
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                                                        14.8%;
30.8%;
                                                                               Conservative
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490 YEDMVVESCGCR 501
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327
345
395
454 AA;
                                                                    Local Similarity
es 96; Conser
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P21274;
CARBOHYD
CARBOHYD
                                 SEQUENCE
                                                        Query Match
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                      CARBOHYD
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MEDLINE; 92378616.
NISHIMATSU S., SUZUKI A., SHODA A., MURAKAMI K., UENO N.;
"Genes for bone morphogenetic proteins are differentially transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 RQAKHKQRKRLKSSCKRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNSTN 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         340 HAIVQTLVNSVNSK-IPKACCVPTELSAISMLYLDENEKVVLKNYQDMVVEGCGCR 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                     PROSITE; FOULD; TGF-beta; 1.
PFAM; PF00619; TGF-beta; 1.
PFAM; PF00688; TGFD_propeptide; 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 394;
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25; Mismatches 25; Indels
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01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
Xenopus More Morbio (Rel. 26, Last annotation update)
Xenopus Jaevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T -> S (IN REF. 2).
QL -> HE (IN REF. 2).
G -> R (IN REF. 2).
N; B055A5A9 CRC32;
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INTERCHAIN (BY SIMILA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                               PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44514 MW;
                                                                             EMBL; L25602; AAB05665.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.6%;
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Best Local Similarity 55.2%;
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3394
3391
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336
1108
1114
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HSSP; P18075; 1BMP.
MGD; MGI:88177; BMP2.
PROSITE; PS00250; TGF_
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294
323
327
358
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Gaps 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 -QRYVFDISALEKDGLL-GAELRILRKKPSDTAKPAAPGGGRAAQLKL--SSCPSGRQPA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 VIPP-YMLDLYHLHSAQLADDQGSSEVDYHMERAASRANTVRSFHHEESMEEIPESGEKT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 VRLLDTRLIH-HNESKWESFDVTPAITRWIAHKQPNHGFVV-EVTHLDNDTNVP-KRHVR 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 -I-SRSLTLDKGHWPRIRPLL---V-TFS-HDGKG-HA-L--HKRQKR-Q-A-RH-KQR- 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : ::| |: : | |: : | |: 335 QVHEKALFLVFGR-TKKRDLFFNEIKARSQQDDKTVYEYLFSQRRKRRAPLATRQGKRPS 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292 KRLKSSCRRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNSTNHAIVQTLV 351
DR HSSP; P18075; 1BMP.

DR PROSITE; PS00250; TGF_BETA; 1.

DR PFAM; PF00068; TGF_DETA; 1.

DR PFAM; PF00068; TGFD_propeptide; 1.

Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.

FT SIGNAL.

FT PROPEP

FT CHAIN

FT DISULFID 298 398 BONE MORPHOGENETIC PROTEIN 2-II.

FT DISULFID 327 395 BY SIMILARITY.

FT DISULFID 331 397 BY SIMILARITY.

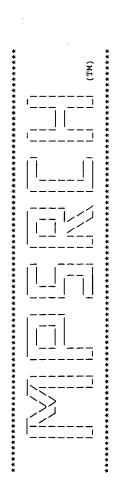
FT DISULFID 331 397 BY SIMILARITY.

FT CARBOHYD 137 137 POTENTIAL.

FT CARBOHYD 202 202 POTENTIAL.

FT CARBOHYD 237 237 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 14.6%; Score 536; DB 1; Length 398;
Local Similarity 34.2%; Pred. No. 5.12e-86;
les 119; Conservative 78; Mismatches 117; Indels 34;
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h completed: Wed Apr 19 19:43:51 2000 J. Lime : 112 secs.



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Wed Apr 19 19:49:04 2000; MasPar time 23.94 Seconds 838.682 Million cell updates/sec Run on:

lar output not generated.

Title:

>US-09-297-092-1 (1-501) from US09297092.pep 3662 1 MRLPKLLTFLLWYLAWLDLE........ANNVVYKQYEDMVVESCGCR 501 Description: Perfect Score: Sequence:

PAM 150 Gap 11 . Scoring table:

122810 seqs, 40068593 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir62 1:pir1 2:pir2 3:pir3 4:pir4 Database:

scale 0.480 Mean 49.502; Variance 103.098; Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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NO.	0.00e+00	00+00	00e+00	.37e-15	74e-13	80e-11	.69e-80	.23e-76	.76e-76	.23e-76	76e-76	.56e-76	.24e-74	.41e-74	24e-74	8.11e-74	1.95e-73	.95e-73	.01e-73	.01e-73	.73e-72	.36e-70	.81e-71
Pred.	0.0	0.0	0.0	4.3	5.74	5.8	2.6	4.2	1.7	4.2	1.7	6.5	5.24	1.4	5.24	8.11	1.9	1.9	3.0	3.01	1.7	1.36	8.8
ption	growth/differentlatio	cartilage-derived mor	bone morphogenetic pr		morphogenetic pr	morphogenetic pr		morphogenetic pr		morphogenetic pr			morphogenetic pr		decapentaplegic prote	morphogenetic pr	morphogenetic pr						
Description	growt	carti	pone	carti	pone	pone	pone	pone	pone	pone	pone	pone	pone	pone	pone	pone	pone	pone	pone	pone	decab	bone	pone
QI QI	JC2347	A55452	S43294	B55452	S43295	S43296	150608	S37073	BMHU2	JH0687	149542	BMHU5	S45355	JH0688	BMHU4	S58791	538343	149541	A49147	JH0689	A26158	150607	JH0801
DB	7	7	7	7	7	7	7	7	Η	7	~	-	7	7	-	7	7	~	~	7	7	7	7
% Query Match Length DB	501	501	495	436	125	151	405	393	396	398	452	454	394	398	408	408	408	420	400	401	588	353	408
% Query Match	100.0	98.5	91.0	25.6	22.7	20.1	15.5	14.9	14.9	14.9	14.9	14.8	14.6	14.6	14.6	14.5	14.5	14.5	14.4	14.4	14.3	14.1	14.1
Score	3662	3608	3332	939	832	735	999	544	546	544	546	543	533	536	533	532	530	530	529	529	525	515	516
Result	-	7	m	4	5	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

5.69e-71	5.04e-70	1.86e-69	1.86e-69	2.23e-67	4.67e-66	1.11e-65	4.67e-66	1.72e-65	2.69e-62	6.39e-62	4.77e-60	3.36e-55	3.36e-55	1.33e-52	1.12e-51	7.29e-52	9.35e-51	3.99e-51	1.82e-49	1.62e-42	3.65e-40
SPDVR1 protein - sea	bone morphogenetic pr	bone morphogenetic pr	osteogenic protein 1	osteogenic protein 2	vgr protein - rat (fr	bone morphogenetic pr	bone morphogenetic pr	Vg-1-related protein	TGF beta homolog dsl-	Vgl embryonic growth	TGF-beta-related prot	bone morphogenetic pr	bone morphogenetic pr	bone morphogenetic pr	GDF-1 embryonic growt	bone morphogenetic pr	growth/differentiatio	GDF-1 embryonic growt	transforming growth f	qene nodal protein -	transforming growth f
S52408	BMHU7	151284	JQ1184	A45056	S37618	JH0690	BMHU6	A54798	A40735	A29619	A43918	153032	BMHU3	JC4646	A39364	JC4838	A46607	C39364	A45402	S29718	S21473
7	Н	7	~	7	7	~	Н	~	7	~	7	7	~	7	7	7	7	7	~	7	7
461	431	313	430	402	207	426	513	510	427	360	455	360	472	476	357	478	366	372	366	354	79
14.1	14.0	13.9	13.9	13.6	13.4	13.4	13.4	13.3	12.9	12.8	12.5	11.8	11.8	11.4	11.3	11.3	11.2	11.2	11.0	9.9	9.6
517	512	509	509	498	491	489	491	488	471	469	459	433	433	419	414	415	409	411	402	364	351
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

1 JC2347 #type complete growth/differentiation factor 5 - human #formal_name Homo sapiens #common_name man 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Apr-1998 IONS JC2347 ICS JC347 ICS JC447 I	CS GDB:BMP9 ##cross-references GDB:433948 trons 211/1 bS glycoprotein E #binding_site carbohydrate (Asn) (covalent) #status predicted\ #182 #length 501 #molecular-weight 55410 #checksum 5334	Query Match 100.0%; Score 3662; DB 2; Length 501; Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 1 MRLPKLLTFLLWYLAWLDLEFICTVLGAPDLGQRPQGTRPGLAKAEAKERPPLARNVFRP 60	GGHSYGGGATNANARAKGGTGOTGCLTOPKKDEPKKLPPRPGGPEPKPCHPPOTRQATAR 120	SDADRKGGNSSYKLEAGLANTITSFIDKGQDDRGPVVRKQRYYFDISALEKDGLLGAELR 240
ENTRY TITLE DATE DATE RECESSIONS REFERENCE #authors #title #title #accession #accession #accession ##resid	ETICS #gene #introns WORDS TURE 189 381-382	Query Match Best Local Matches 5 1 MRL 1 MRL	61 GG 61 GG 121 TT 121 TT	181 SI 181 SI
RESULT ENTRY TITLE ORGANISM DATE ACCESSION REFERENCE # journ # journ # title #	GENETICS # gene # in tr # in tr KEYWORDS FEATURE 189 381-3	Que Bes Mat Db	Oy Oy Oy	op Oy

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#authors Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Rybak, N.J.P.; Kozak, C.A.; Reddi, A.H.; Moos Jr., M. Fjournal J. Biol. Chem. (1994) 269:2827-28234

#title Cartilage-derived morphogenetic proteins. New members of the transforming growth factor-beta superfamily predominantly expressed in long bones during human embryonic development.
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               RNFKNSAQLCLELEAWERGRAVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA
                                                                                                                  RSGQDDKTVYEYLFSQRRKRRAPLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIA
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##cross-references GB:U13660; NID:g600731; PID:g600732
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Y #length 501 #molecular-weight 55640
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Pred. No. 0.00e+00;
4; Mismatches 4.
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1 Similarity 98.4%;
493; Conservative
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#formal_name Mus musculus #common_name house mouse
20-oct-1994 #sequence_revision 10-Nov-1995 #text_change
17-Mar-1999
RSGQDDKTVYEYLFSQRRKRRAPSATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIA
            PLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID
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Pred. No. 0.00e+00;
23; Mismatches 15; Indels
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#journal Nature (1994) 368:639-643

#title Limb alterations in brachypodism mice due new member of the TGF-beta-superfamily.
#cross-references MUID:94195427
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##residues 1-495 ##label
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#cross-references MUID:94195427
#accession S43295
                                   ##molecule_type DNA
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                                                                                                                                                                                      Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak, C.A.; Reddi, A.H.; Moos Jr., M. J. Biol. Chem. (1994) 269:28227-28234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
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                                                                                                                                                                                                                                                                                                                              preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J. Mature (1994) 308:639-643. Limb alterations in brachypodism mice due to mutations in new member of the TGF-beta-superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S43295 #type fragment bone morphogenetic protein homolog GDF6 precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRPPQQPEAREPPGRGPRLVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 VAPAA---GSA-E-PGPAGAPRPGWEVFDVWRGLRP-QPWKQLCLELRAAWGGEPGAAED 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARTPGPQQPPPPDLRSLGFGRRVRTPQERALLVVFSRSQRKTLFAEMREQLGSATEVVG 279
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                                                                                (fragment)
#formal_name Bos primigenius taurus #common_name cattle
10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #formal_name Mus musculus #common_name house mouse
20-Oct-1994 #sequence_revision 07-Feb-1997 #text_change
17-Mar-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 RSG-QDDK-----TVY-EY-LFSQR--RKRRAPLATRQGKRPSKNLKARCSRKA
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                                                     B55452 #type fragment cartilage-derived morphogenetic protein 2 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 436;
                                                                                                                                                                                                                                                                                                                                                           ##residues 1.436 ##label CHA
##cross-references GB:U13661; NID:9632489; PID:9632490
:X #length 436 #checksum 3177
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 939; DB 2; Le
Pred. No. 4.37e-153;
85; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400 CCVPTKLTPISILYIDAGNNVVYNEYEEMVVESCGCR 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            growth and differentiation factor
                                                                                                                                                                                                                                                                                            #cross-references MUID:95050604
#accession B55452
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Local Similarity 47.6%;
Les 189; Conservative
                                                                                                                                  17-Mar-1999
B55452
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predicted #label PPR\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Francis, P.H.; Richardson, M.K.; Brickell, P.M.; Tickle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 543296 #type complete
bone morphogenetic protein-related protein (GDF7) - mous
#formal_name Mus musculus #common_name house mouse
20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change
17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150608 #type complete
bone morphogenetic protein 4 - chicken
#formal_name Gallus gallus #common_name chicken
13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
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                                                                                                                                                    #product bone morphogenetic protein homolog GDF6
  (fragment) #status predicted #label MAT
#length 125 #checksum 8499
                                                                                                                                                                                                                                                                                                                                        RRRRRTAFASRHGKRHGKKSRLRCSRKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFP
                                                                                                                                                                                                                                                                                                                                                                                 377 RRKRRAPLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-151 ##label STO
#length 151 #molecular-weight 15697 #checksum 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, Kingsley, D.M.; Lee, S.J.
Nature (1994) 368:639-643
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Pred. No. 5.80e-113;
                                                                                                                                                                                                                                                  Length 125;
##residues 1-125 ##label STO
##cross-references EMBL:U08338; NID:9488463; PID:9488464
                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
                                                                                                                                                                                                                                             Score 832; DB 2; L
Pred. No. 5.74e-132;
22; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24; Mismatches
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ilarity 74.3%;
Conservative
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Best Local Similarity 79.2%;
Matches 99; Conservative
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M.; Nakanishi, T.; Kobayashi, J.; Nakazato, H.
J. Biochem. (1994) 115:279-285
Expression and characterization of human bone morphogenetic
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                                                                                                                                                                                                                                                                                                 280 VRSVPGLDGSGWEVFDIWKLFRNFKNSAQLCLELEAWERGRAVDLRGLGFDRAARQVHEK 339
399 RCSRKALHVNFKDMGWDDMIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDP 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                     340 ALFL-VFGRTKKRDLFFNEIKARSGQDDKTVYEYLFSQRRKRRAPLATRQGKRPSKNLKA 398
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Bombyx mori nuclear polyhedrosis virus.
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its hormone is capable of inducing bone formation at ectopic
morphological locations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hewick, R.M.; Wang, E.A. Science (1988) 242:1528-1534
                                                                                                        FFNLSSVPTDEFLTSAELQIFREQMQEALGNSSFQHRINIYEIIKPATASSKFPVTRLLD
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                                                                                                                                                                                                                                              TRLVTQ-NTSQWESFDVTPAVMRWTAQGHTNHGFVV-EVAHLEEKPGVS-KRHVR-I-SR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 SCKRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNSTNHAIVQTLVNSVNS
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##residues 1-396 ##label WO2
##cross-references GB:M22489; NID:g179501; PID:g179502
SNCE PC2178 "...... W . Kanava T.; Shime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #formal_name Homo sapiens #common_name man
16-Sep-1992 #sequence_revision 03-Aug-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bone morphogenetic protein 2 precursor bone morphogenetic protein 2A; rhBMP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352 K-IPKACCVPTELSAISMLYLDENEKVVLKNYQDMVVEGCGCR
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##residues 290-295,'X',297-304 ##label ISH
##experimental_source cell line BoMo-15AIIc
NGE A56729
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ap_position 20p12-20p12
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                                Bone morphogenetic proteins and a signalling pathway that controls patterning in the developing chick limb.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 P-SYMLDLYRLQSGEEEERSLQEISLQYPERSASRANTVRSFHHEEHLESVPGPSEAPRI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RFVFNLSSVPDNEVISSEELRLYREQVEEPSAAWERGFHRINIYEVMKPLSERSQAITRL 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 I-SRSLPQGHGGDWAQL-RPLLVTFGHDGRG-HA-L-T-RRARRSP--KHHGSR--KN-K 302
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bone morphogenetic protein 2 - rat
#formal_name Rattus norvegiuus #common_name Norway rat
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feng, J.Q.; Chen, D.; Feng, M.; Harris, M.A.; Mundy, Harris, S.E. submitted to the EMBL Data Library, September 1993 CDNA sequence of fetal rat calvarial osteoblast bone morphogenetic protein 2.
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                                                                                                                                                                         preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 2.69e-80;
89; Mismatches 152; Indels
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Pred. No. 4.23e-76;
Development (1994) 120:209-218
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ilarity 32.2%;
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#product bone morphogenetic protein 2, long form #status
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#journal Biochem. Biophys. Res. Commun. (1992) 186:1487-1495
#title Genes for bone morphogenetic proteins are differentially
#cross-references MUID:92378616
#accession JH0687
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Biochim. Biophys. Acta (1991) 1089:280-282
cDNA sequence of Xenopus laevis bone morphogenetic protein
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#modified_site pyrrolidone carboxylic acid (Gln) (in
mature form) #status experimental\
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##residues 1-398 ##label NIS
##cross-references GB:X63424; NID:g64585; PID:g64586
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NCE $16244
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                                                                                                                                                                                                               #length 396
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King, J.A.; Marker, P.C.; Seung, K.J.; Kingsley, D.M.
Dev. Biol. (1994) 166:112-122
BMP5 and the molecular, skeletal, and soft-tissue alterations
                                                                                                                        #product bone morphogenetic protein 21 #status predicted
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                                                                                                                                               #label MAT\
#blading_aite carbohydrate (Asn) (covalent) #status
predicted
#length 398 #molecular-weight 45586 #checksum 9563
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#formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
23-Feb-1997
149542
                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 PLLVTFSHDGKG-HA-L--HKRQKR-Q-A-RH-KQR-KRLKSSCRRHPLYVDFSDVGWND
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#length 452 #molecular-weight 51511 #checksum 1308
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                                                                                                                                                                                                                                                                                                                     88; Mismatches 136; Indels 35;
##residues 1-6,'S',8-15,'V',17-232,'N',234-398 ##label
##cross-references EMBL:X55031; NID:g64581; PID:g64582
FICATION #superfamily inhibin
DS dimer; glycoprotein
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##cross-references GB:L41145; NID:9755033; PID:9755034
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Pred. No. 4.23e-76;
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Best Local Similarity 28.8%; Pred. No. 1.76e-76;
Matches 107; Conservative 101; Mismatches 140;
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#accession I49542
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Best Local Similarity 32.7%;
Matches 126; Conservative
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#domain propeptide #status predicted #label PRO\
#product bone morphogenetic protein 5 #status predicted
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Proc. Natl. Acad. Sci. U.S.A. (1990) 87:9843-9847
Identification of transforming growth factor beta family members present in bone-inductive protein purified from bovine bone.
                                                                                                                                                                                                                                                                                               30 EGLCEFPLRSHLEPTNHAVIQTLANSMDPESTPPTCCVPTRLSPISILFIDSANNVYKQ 489
141 PSSFLLKKAREPGPPREPKEPFRPPITPHEYMLSLY-RT-LS-DADRKGGNSSVKLEAG 197
                                    -ADMVMSFVNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDKGNHRFENE 210
                                                        211 TIKIS-IYQI-IKEY-TNRDADLFLLDTRKTQALD-VGWLVFDITVTSNHWVINPQNNLG 266
                                                                                                                                                    254 APGGGRAAQLKLSSCPSGRQPA-SLLDVRSVPGLDGSGWEVFDIWKLFRNF-KNS-AQLC 310
                                                                                                                                                                                             LQLCAETGDGRSINVKSAGLV-GRHGPQSKQPFMV-AFFKASEVLLRSVRAASKRKNQNR 324
                                                                                                                                                                                                                                   311 LEL-EAWERGRAVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKTV 369
                                                                                                                                                                                                                                                                       325 NKSN-SHQDPSRMP-SA--GDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYAAFYC 380
                                                                                                                                                                                                                                                                                                                                                   381 DGECSFPLNAHMNATNHAIVQTLVHLMFPDHVPKPCCAPTKLNAISVLYFDDSSNVILKK 440
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predicted
#length 454 #molecular-weight 51736 #checksum 4416
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#type complete
bone morphogenetic protein 5 precursor - human
#formal_name Homo sapiens #common_name man
18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change
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Pred. No. 6.56e-76;
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#map_position 6pter-6qter
CLASSIFICATION #superfamily inhibin
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hes 96; Conservative
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490 YEDMVVESCGCR 501
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Feng, J.O.; Harris, M.A.; Ghosh-Choudhury, N.; Feng, M.; Mudy, G.R.; Harris, S.E.
Blochim. Blophys. Acta (1994) 1218:221-224
Structure and sequence of mouse bone morphogenetic protein-2 gene (BMP-2): comparison of the structures and promoter regions of BMP-2 and BMP-4 genes.
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30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
08-Sep-1997
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                             JH0688 #type complete
bone morphogenetic protein 2II precursor - African clawed
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270 QLCAETGDGRSINVKSAGL - - VGRQGPQSKQPFMV - AFFKASEVLLRSVRAANKRKNQNR 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bone morphogenetic protein-2 - mouse
#formal_name Mus musculus #common_name house mouse
10-Dec-1994 #sequence_revision 17-Nov-1995 #text_change
                                                                                                    327 NKS-SSHQDSSR--MSSV-GDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYAAFYC
                                                                                                                                                                                                           DGECSFPLNAHMNATNHAIVQTLVHLMFPDHVPKPCCAPTKLNAISVLYFDDSSNVILKK
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#length 394 #molecular-weight 44509 #checksum 1098
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##residues 1-398 ##label NIS
##rcoss-references GBX63425; NID:g64583; PID:g64584
##experimental_source occyte
CLASSIFICATION #superfamily inhibin
KEYWORDS glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 533; DB 2; I
Pred. No. 5.24e-74;
25; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *type complete
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#accession JH0688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 14.6%;
Best Local Similarity 55.2%;
Matches 64; Conservative
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                                                                                                                                                                                                                                                                                                             443 YRNMVVRSCGCH 454
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490 YEDMVVESCGCR 501
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#domain signal sequence #status predicted #label SIG\
#domain propeptide #status predicted #label PRO\
#product bone morphogenetic protein 4 #status predicted
#label MAT\
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                                                                                                                                                                                                                                                                131 IQRFFFNLSSIPDEELVTSSELRIFREQVQEPFKTDGSKLHRINIYDIVKPAAAASRGPV 190
                                                                                                                                                                                                                                                                                                                                                      191 VRLLDTRLIH-HNESKWESFDVTPAITRWIAHKQPNHGFVV-EVTHLDNDTNVP-KRHVR 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 -SLLDVRSVPGLDGSGWEVFDIWKLFRNFKNSAQLCLELEAWERGRAVDLRGLGFDRAAR 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 -I-SRSLTLDKGHWPRIRPLL---V-TFS-HDGKG-HA-L--HKRQKR-Q-A-RH-KQR- 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 KRLKSSCRRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNSTNHAIVQTLV 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #product bone morphogenetic protein 2II #status
predicted #label MAT\
10 #blnding_site carbohydrate (Asn) (covalent) #status
predicted
#length 398 #molecular-weight 45616 #checksum 1620
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predicted
#length 408 #molecular-weight 46555 #checksum 48
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bone morphogenetic protein 4 precursor - human
bone morphogenetic protein 2B
#formal_name Homo sapiens #common_name man
15.5ep-1992 #sequence_revision 03-Aug-1995 #text_change
237278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78; Mismatches 117; Indels 34;
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Best Local Similarity 52.0%; Pred. No. 5.24e-74;
Matches 65; Conservative 31; Mismatches 26; Indels
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##cross-references GB:M22490; NID:g179503; PID:g179504
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##cross-references GDB:125205; OMIM:112262
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CLASSIFICATION #superfamily
KEYWORDS bone; glyco
FEATURE
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ALTERNATE_NAMES
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293-408
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Apr 19 19:52:19 2000; MasPar time 10.53 Seconds 632.638 Million cell updates/sec ar output not generated. Run on:

>US-09-297-092-1 (1-501) from US09297092.pep 3662 1 MRLPKELTFLLWYLAWLDLE......ANNVVYKQYEDMVVESCGCR 501 Title:

Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

Searched:

134018 segs, 13297625 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT9_COMB 5:backfiles1

scale 0.205 Mean 34.368; Variance 167.251; Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		8					
Score		Match	Match Length DB	BB	a	Description	Pred. No.
3662		100.0	501	7	US-08-288-	Sequence 2, Applicatio	0.00e+00
3332		91.0	495	7	US-08-455-	10,	1.15e-278
3332		91.0	495	4	PCT-US94-0	Sequence 10, Applicati	1.15e-278
904		24.7	120	7	US-08-362-	4, A	2.05e-65
904		24.7	120	4	PCT-US94-1	4	2.05e-65
903		24.7	321	4	PCT-US94-1	26,	2.50e-65
903		24.7	321	~	US-08-362-	Sequence 26, Applicati	2.50e-65
895		24.4	119	1	US-08-455-	13,	1.23e-64
892		24.4	119	4	PCT-US94-0	13,	1.23e-64
849	_	23.2	263	7	US-08-362-	Sequence 32, Applicati	1.14e-60
84	6	23.2	263	4	PCT-US94-1	Sequence 32, Applicati	1.14e-60
832	~	22.7	134	4	PCT-US94-0	e, A	3.32e-59
832	~	22.7	134	П	US-08-581-	Sequence 6, Applicatio	3.32e-59
815		22.3	388	4	PCT-US94-1	Sequence 34, Applicati	9.63e-58
815	'n	22.3	388	Н	us-08-362-	34,	9.63e-58
79	'n	21.7	411	Н	US-08-362-	Sequence 28, Applicati	5.05e-56
79	'n	21.7	411	4	PCT-US94-1	28,	5.05e-56
790	0	21.6	119	-	US-08-581-	Sequence 7, Applicatio	1.36e-55
79	0	21.6	119	4	PCT-US94-0	Sequence 7, Applicatio	1.36e-55
78,	Ψ.	21.4	102	7	US-08-288-	Sequence 13, Applicati	4.45e-55
784		21.4	102	-	US-08-335-	Sequence 51, Applicati	4.45e-55
741	_	20.2	129	Н	us-08-360-	Sequence 15, Applicati	2.18e-51
741		20.5	129	П	US-08-741-	Sequence 13, Applicati	2.18e-51

2.18e-51 18e-51 7.112e-51				
Sequence 2, Applicatio Sequence 7, Applicatio Sequence 7, Applicatio Sequence 6, Applicatio Sequence 6, Applicatio Sequence 30, Applicatio Sequence 30, Applicatio Sequence 10, Applicatio Sequence 15, Applicatio Sequence 15, Applicatio Sequence 5, Applicatio Sequence 10, Applicatio Patent No. 5166058.		n 		ud lige hael GROWTH/DIFFERENTIATING FACTOR OF TGF- FAMILY TGF- FAMILY TGF- FAMILY TGF- FAMILY Street N.W. Suite 330 Kitible NS/MS-DOS ease #1.0, Version #1.25 \$\frac{9}{9}\text{4}\$ \$\frac{9}{9}\text
PCT-US94-1 US-08-562- DCT-US94-0 US-08-581- US-08-581- US-08-581- US-08-581- US-08-581- US-08-681- SIGNOSO-5 SIGNOSO-5 SIGNOSO-5 SIGNOSO-3 SIGNOSO-3 SIGNOSO-3 SIGNOSO-3 US-08-449- US-08-449- US-08-449- US-08-449- US-08-449- US-08-449- US-08-449- US-08-449- US-08-449- US-08-449- US-08-449- US-08-449- US-08-449- US-08-147- US-08-09-98-4	IGNMEN	STANDAND, FALL	US/08288508C	equence 2, Application US/08288508C Satent No. 5930094 GENERAL INFORMATION: APPLICANT: H tren, Gertrud APPLICANT: H tren, Gertrud APPLICANT: H tren, Gertrud APPLICANT: PAULISTE, MICHEL TITLE OF INVENTION: THE TGF-FAMILY NUMBER OF ESCHOREES: ADDRESSEE: NARAIGO, Marmelstein, M. STREET: 655 Fifteenth Street N.W. SCITY: Washington STATE: D.C. COUNTRY: U.S.A. ZIP: 20005-5701 COMPUTER: ENDAPE: PCOMPAINE MEDIUM TYPE: Floppy disk COMPUTER: TBM PC COMPAINE COMPUTER: TBM PC COMPAINE MEDIUM TYPE: PATENTIN Release #1.0, VG CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/288,508C FILING DATE: 10-AUG-1993 RION APPLICATION NUMBER: DE P 44 18 222 FILING DATE: 10-AUG-1993 RION APPLICATION NUMBER: DE P 44 18 222 FILING DATE: 25-MAY-1994 RAPLICATION NUMBER: DE P 44 18 222 FILING DATE: 25-MAY-1994 ATPORMATION NUMBER: DE P 44 18 APPLICATION NUMBER: DE P 44 18 FILING DATE: 10-AUG-1993 APPLICATION NUMBER: DE P 44 18 APPLICATION NUMBER: DE P 44 18 ATPORMATION NUMBER: DE P 44 18 ATPORT APPLICATION NUMBER: DE P 44 1019
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22000.22 2000.11 11.000.00 11.000.00 11.000.00 11.000.00 11.000.00 11.000.00 11.000.00	1	7 - 2805	2, Appli	Sequence 2, Application US/082 Patent No. 5994094 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: H tten, Gertrud APPLICANT: Paulista, Micha TITLE OF INVENTION: THE TG: NUMBER OF SEQUENCES: 40 CORRESPONDENCES: 40 CONTRES: 10 STREET: 655 Fifteenth St. CIT: Washington STREET: G55 Fifteenth St. CIT: Washington STATE: D.C. COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: EBADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: EBADABLE FORM: MEDIUM TYPE: PatentIn Relea COMPUTER: IBM CC-DOS SOFTWARE: PAPLICATION DATA: APPLICATION NUMBER: US/OF FLING DATE: 10-AUG-1994 CLASSIFICATION DATA: APPLICATION NUMBER: DE P FILING DATE: 10-AUG-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: DE P FILING DATE: 25-MAY-1994 PRIOR APPLICATION NUMBER: DE P FILING DATE: 09-JUN-1994 ATTORNEY/AGENT INFORMATION: NAME: JAHNS, KTISTINA M. REGISTRATION NUMBER:
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                                                                                                                                                                                                                                     61 GGHSYGGGATNANARAKGGTGQTGGLTQPKKDEPKKLPPRPGGPEPKPGHPPQTRQATAR 120
                                                                                                                                                                                                                                                                      TVTPKGQLPGGKAPPKAGSVPSSFLLKKAREPGPPREPKEPFRPPPITPHEYMLSLYRTL 180
                                                                                                                                                                                                                                                                                                                    SDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR 240
                                                                                                                                                                                                                                                                                                                                                                 ILRKKPSDTAKPAAPGGGRAAQLKLSSCPSGRQPASLLDVRSVPGLDGSGWEVFDIWKLF 300
                                                                                                                                                                                                                                                                                                                                                                                                            RNFKNSAQLCLELEAWERGRAVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSGQDDKTVYEYLFSQRRKRRAPLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID 480
                                                                                                                                                                                        1 MRLPKLLTFLLWYLAWLDLEFICTVLGAPDLGQRPQGTRPGLAKAEAKERPPLARNVFRP 60
                                                                                                                                                      Gaps
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                                                                                                                              Length 501;
                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: LEE, SE-JIN
APPLICANT: HUWH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         495 AA.
                                                                                                                             Query Match 100.0%; Score 3662; DB 2; Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 501; Conservative 0; Mismatches 0
                                                                                        MOLECULE TYPE: protein
JENCE 501 AA; 55410 MW; 1235559 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/08455559 Patent No. 5801014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/08455559
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
                  INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 501 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481 SANNVYKQYEDMVVESCGCR 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SANNVYKQYEDMVVESCGCR 501
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                                                                      amino acid
                                                                                 linear
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US-08-455-559-10
                                                                              TOPOLOGY:
                                                                                                        SEQUENCE
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SDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPAVRKQRYVFDISALEKDGLLGAELR 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GGHIYGVGATNA--RAKGSSGQT----QAKKDEPRKMPPRSGGSETKPGPSSQTRQAAAR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 TVTPKGQLPGGKASSKAGSAPSSFLLKKTREPGTPREPKEPFRPPPITPHEYMLSLYRTL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRLPKLLTLLLWHLAWLDLELICTVLGAPDLGQRTPGAKPGLTKAEAKERPPLARNVFRP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 3332; DB 1; Length 49
Pred. No. 1.15e-278;
23; Mismatches 15; Indels
                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                        SOFTWAKE: PETENTIN KELGASE #1.0, VET
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,559
FILING DATE: 31-MAY-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/003,144
FILING DATE: 12-34-1993
ATTORNEY AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R. REGISTRATION NUMBER: 31,678
REGISTRATION NUMBER: 31,678
REECENAMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 11 near
MOLECULE TYPE: protein
ENCE 495 AA; 54885 MW; 1212056 CN;
                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             495 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 91.0%;
Local Similarity 91.2%;
hes 457; Conservative
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SANNVYKQYEDMVVESCGCR
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US-09-297-092-1.rai

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61 EPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVYYKQYEDMVVESCGCR 120
                                                 421 PLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 RSGQDDKTVYEYLFSQRRKRRAPLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIA 420
                                 415 PLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 APLATROGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHL 60
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Best Local Similarity 100.0%; Pred. No. 2.05e-65;
Matches 120; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Wozney, John
APPLICANT: Wolfman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
WUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: December 22, 1994
CLASSIFICATION: 514
                                                                                                                                                                                                       120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENETICS INSTITUTE, INC.
                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REGISTRATION TOWNER: 5202-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
ENCE 120 AA; 13581 MW; 77978 CN;
                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08362670B
Patent No. 5658882
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08362670B
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INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                  475 SANNVYKQYEDMVVESCGCR 495
                                                                                                                                                                                                       STANDARD;
                                                                                                                      SEQUENCE CHARACTERISTICS LENGTH: 120 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             617 876-5851
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                                                                                                                                                                                                       US-08-362-670B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPAVRKQRYVFDISALEKDGLLGAELR 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSGQDDKTVYEYLFSQRRKRRAPLANRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GGHIYGVGATNA--RAKGSSGQT----QAKKDEPRKMPPRSGGSETKPGPSSQTRQAAAR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 ILRKKPLDVAKPAVPSSGRVAQLKLSSCPSGRQPAALLDVRSVPGLDGSGWEVFDIWKLF 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRLPKLLTLLLWHLAWLDLELICTVLGAPDLGQRTPGAKPGLTKAEAKERPPLARNVFRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Gaps
                                                                                                                               APPLICANT: SE-JIN LEE
APPLICANT: HUYNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 3332; DB 4; Length 495;
Pred. No. 1.15e-278;
23; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00657
FILING DATE: 1/12/94
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FD3256 CIP OF PD2280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD3256 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFRAX: 619-455-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 495 AA; 54885 MW; 1212056 CN;
                                                                                                  Sequence 10, Application PC/TUS9400657 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                 Sequence 10, Application PC/TUS9400657
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 495 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 91.0%;
Best Local Similarity 91.2%;
Matches 457; Conservative
                                                                                                                                                                                                                                                                                                          9006
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 XXXXXX
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62 -LLDARTLDPQGAPPAGWEVFDVWQGLRH-QPWKQLCLELRAAWGELDAGEAEARARGPQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 OPPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGSAEAAGPGAGAEGSW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            323 ----DLRGLGFDRAARQVHEKALFLVFGRTKKRDLF--FNE-1---KA--R-SGQDDK- 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 ---TVY-E---YLFSQ-RRKRRAPLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWII 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 LRRQKYLFDVSMLSDKEELVGAELRLFRQAPS--A-PWGPPAG-PLHVQLFPCLS---PL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 PPPSGAPDARPWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 24.7%; Score 903; DB 4; Length 321;
Best Local Similarity 52.5%; Pred. No. 2.50e-65;
Matches 169; Conservative 61; Mismatches 46; Indels 46;
                                                             Sequence 26, Application PC/TUS9414030A
GENERAL INFORMATION:
APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lazar, Steven R.
REGISTRATION UNUBER: 32,618
REFERENCE/DOCKET NUMBER: 5202D-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEPHONE: 617 498-851
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,103
FILING DATE: 07-DEC-1993
APPLICATION NUMBER: US 08/217,780
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 08/333,576
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US94/14030A
FILING DATE: Herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
ENCE 321 AA; 35823 MW; 512809 CN;
                                Sequence 26, Application PC/TUS9414030A
                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                                          ADDRESSEE: GENETICS INSTITUTE, STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 321 amino acids amino acid
                                                                                                                                                                                                                                            Massachusetts
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                          CLITY: Cambridge
STATE: Mass
                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                           ZIP: 02140
                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 2.05e-65;
0; Mismatches 0; Indels
                                                                                                                                                                                    Sequence 4, Application PC/TUS9414030A
GENERAL INFORMATION:
APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 AA
                                                120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,103
FILING DATE: 07-DEC-1993
APPLICATION NUMBER: US 08/217,780
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 08/333,576
FILING DATE: 02-NUV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US94/14030/
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202D-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEPRAX: 617 876-5851
                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SQUENCE 120 AA; 13581 MW; 77978 CN;
                                                                                                                                                     Sequence 4, Application PC/TUS9414030A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                               CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 24.7%;
Best Local Similarity 100.0%;
Matches 120; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T 6
PCT-US94-14030A-26
                                T 5
PCT-US94-14030A-4
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Gaps 22;

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368 ---TVY-E---YLFSQ-RRKRRAPLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWII 419
                                    240 APLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYI 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.4%; Score 895; DB 1; Length 119; 99.2%; Pred. No. 1.23e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CALP: 9000,
CADDUTER: ELOPPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: ELD PP Compatible
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NOMER: 02/08/455,559
FILING DATE: 31-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFOMMATION:
REGISTRATION NUMBER: 31,678
REGISTRATION NUMBER: DP2280
TELEPHONE: 619/455-5100
TELEPHONE: 619/455-510
INFORMATION FOR SEO ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 11,19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LEE, SE-JIN
APPLICANT: HUXNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                       119 AA
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                                                                                                                                                                                                         PRT;
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119 AA; 13523 MW; 76702 CN;
                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/08455559 Patent No. 5801014 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/08455559
                                                                                                    300 DAGNNVVYKQYEDMVVESCGCR 321
                                                                                                                      480 DSANNVYKQYEDMVVESCGCR 501
                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 99.2%;
Matches 118; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 OPPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGSAEAAGPGAGAEGSW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 24.7%; Score 903; DB 1; Length 321;
Best Local Similarity 52.5%; Pred. No. 2.50e-65;
Matches 169; Conservative 61; Mismatches 46; Indels 46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 LRRQKYLFDVSMLSDKEELVGAELRLFRQAPS--A-PWGPPAG-PLHVQLFPCLS---PL 61
                                                                                                                                                                                                                                                                 APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Wozney, John
APPLICANT: Wolfman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLING DATE: US/08362,670B
FILLING DATE: December 22, 1994
                                                                                   321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: GENETICS INSTITUTE, INC. STREET: 87 CambridgePark Drive
                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
JENCE 321 AA; 35823 MW; 512809 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                     Sequence 26, Application US/08362670B
Patent No. 5658882
                                                                                                                                                                                    Sequence 26, Application US/08362670B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 11-01
480 DSANNVYKQYEDMVVESCGCR 501
                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                   Patent No. 5658882
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: De CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                               US-08-362-670B-26
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STANDARD;

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US-08-362-670B-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGCR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 PLANRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLE 60
                            443 PINHAVIQTLANSMDPESTPPTCCVPTRLSPISILFIDSANNVVYKQYEDMVVESCGCR 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 119;
                                                                                                                                             Sequence 13, Application PC/TUS9400657
GENERAL INFORMATION:
APPLICANT: SE-JIN LEE
APPLICANT: HUYNH, THANH
TITLE OF INVERTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                              ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/00657

FILING DATE: 1/12/94
                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD3256 CIP OF PD2280
TELECOMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                  ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                         Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 895; DB 4; I
Pred. No. 1.23e-64;
0; Mismatches 1;
                                                                         119
                                                                         PRT;
                                                                                                                              Sequence 13, Application PC/TUS9400657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..119
CE 119 AA; 13523 MW; 76702 CN;
                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 24.4%;
Best Local Similarity 99.2%;
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Protein
                                                               RESULT 9
ID PCT-US94-00657-13
                                                                                                                                                                                                                                                        COUNTRY:
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Gaps 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 V-Y-E---YLFSQ-RRKRRAPLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 SGSPDTGSWLPSPGRRRRTAFASRHGKRHGKKSRLRCSRKPLHVNFKELGWDDWIIAPL 184
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Pred. No. 1.14e-60;
41; Mismatches 25; Indels 14;
                                                                                                                                                                                                         APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Wozney, John
APPLICANT: Wolfman, Neil
APPLICANT: Wolfman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Thomsen, Transen, Gerald H.
APPLICANT: Thomsen, Transen, Transen, Transen, Transen, Transen, Transen, Transen, Transen, Tansen, Tans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONTUIDE: LAW TO CONTUIDE: LAW STATEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,670B FILLIG DATE: December 22, 1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: GENETICS INSTITUTE, INC. STREET: 87 CambridgePark Drive CITY: Cambridge STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
JENCE 263 AA; 29183 MW; 354042 CN;
                                                                                       Sequence 32, Application US/08362670B
Patent No. 5588882
GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
Sequence 32, Application US/08362670B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202
TELECOMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEPHONE: 617 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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Local Similarity 59.8%;
hes 119; Conservative
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PCT-US94-14030A-32
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STANDARD;
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US-08-581-529B-6
PCT-US94-07762-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 263;
                                                                                                                   APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: BRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: GENETICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14030A
FILING DATE: Herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 23.2%; Score 849; DB 4; Le
Best Local Similarity 59.8%; Pred. No. 1.14e-60;
Matches 119; Conservative 41; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,103
FILING DATE: 07-DEC-1993
APPLICATION NUMBER: US 08/217,780
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 08/33,576
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: LAZAT, STEWEN R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202D-PCT
TELECHONE: 617 498-8260
TELEPHONE: 617 498-8260
TELERAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
                                                                                            Application PC/TUS9414030A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 263 AA; 29183 MW; 354042 CN;
                                                                  Sequence 32, Application PC/TUS9414030A
                                                                                                                                                                                                                                            245 NNXVYKQYEDMVVESCGCR 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 87 Cambridger
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
                                                                                          Sequence 32, Applicat GENERAL INFORMATION:
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RESULT

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70 LRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVE 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                  Sequence 6, Application PC/TUS9407762
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INFORTION: GROWTH DIFFERENTIATION FACTOR-6
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
PTLING DATE: 08-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 AA.
                                                                                                                                                  ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: TUMARKIN, LISA A., PH.D.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: FD2349
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
JENCE 134 AA; 15226 MW; 97138 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08581529B
Patent No. 5770444
GENERAL INFORMATION:
Sequence 6, Application PC/TUS9407762
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amino acid
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Matches 99; Conservative
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122 TCPGAARAPRLLYSRAAEPLVGQRWEAFDVADAMRRHRREPRPPRAFCLLLIRAVAGPVPS 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 GTGTASPRAVIGGRRRRRTALAGTRTAQGSGGGAGRGHGRRGRSRCSRKPLHVDFKELGW 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ::: ||::||:|| || || || || 367 -K-TVYE-YLFSQRRKRRAPLA-TR--QGK----R-PSKNLKARCSRKALHVNFKDMGW 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 DDWIIAPLDYEAYHCEGLCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCCVPARLSPI 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322 -VDLRGLGFDRAA----RQVHEKALFLVFGRTKKRDLFFNEIKA--RS-GQ----D---D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 815; DB 4; Length 388;
Pred. No. 9.63e-58;
84; Mismatches 60; Indels 36;
                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 AA.
                                                                                                                       APPLICATION NUMBER: PCT/US94/14030A
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                        NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202D-PCT
                                                                                                                                                                                           APPLICATION NUMBER: US 08/164,103
FILING DATE: 07-DEC-1993
APPLICATION NUMBER: US 08/217,780
                                                                                                                                                                                                                                                  FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 08/333,576
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
ENCE 388 AA; 42118 MW; 683274 CN;
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 34, Application US/08362670B
Patent No. 5658882
GENERAL INFORMATION:
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TELEPHONE: 617 498-8260
                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 22.3%;
Best Local Similarity 45.0%;
Matches 147; Conservative
                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
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377 RRKRRAPLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFP 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 LRSHLEPINHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 RRRRRTAFASRHGKRHGKKSRLRCSRKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFP 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 832; DB 1; Length 134; Pred. No. 3.32e-59; 22; Mismatches 4; Indels
                                                                                                                                                                                                                                                             SOFTWARE PATENTIN Release #10, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,529B
FILING DATE: 15-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET VUMBER: 07265/082001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEPAS: (619) 678-5070
TELEPAS: (619) 678-5070
TELEPAS: (619) 678-5070
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 34, Application PC/TUS9414030A
GENERAL INFORMATION:
APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
              APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
NUMBER OF SUGENCE: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388 AA
                                                                                ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
CITY: La JOlla
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34, Application PC/TUS9414030A
                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
FENCE 134 AA; 15226 MW; 97138 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 134 amino acids TYPE: amino acid
                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 22.7%;
Best Local Similarity 79.2%;
Matches 99; Conservative
APPLICANT: Lee, Se-Jin
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ID PCT-US94-14030A-34
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Gaps

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Query Match 22.3%; Score 815; DB 1; Length 388;
Best Local Similarity 45.0%; Pred. No. 9.63e-58;
Matches 147; Conservative 84; Mismatches 60; Indels 36; Gaps 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 PLALRRLGFGWPGGGGSAAEERAVLVVSSRTQRKESLFREIRAQARALGAALASEPLPDP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 -K-TVYE-YLFSQRRKRRAPLA-TR--QGK----R-PSKNLKARCSRKALHVNFKDMGW 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 RSPADESAAETGQSFLFDVSSLNDADEVVGAELRVLRRGSPESG-PGSWTS--PPLLLLS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 TCPGAARAPRLLYSRAAEPLVGQRWEAFDVADAMRRHRREPRPPRAFCLLLLRAVAGPVPS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 GTGTASPRAVIGGRRRRTALAGTRTAQGSGGAGRGHGRRGRSRCSRKPLHVDFKELGW 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 DDWIIAPLDYEAYHCEGLCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCCVPARLSPI 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WOZNEY, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Wolfman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION 104 PATE:
APPLICATION 105 PATE:
APPLICATION: 514
                                                                                                                                             E: GENETICS INSTITUTE, INC. 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
TYPE: Jinear
MOLECULE TYPE: Drotein
SEQUENCE 388 AA; 42118 MW; 683274 CN;
                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-D
TELECOMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
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                                                                                                                                                                                                Massachusetts
                                                                                                                                              ADDRESSEE: GENETI
STREET: 87 Cambri
CITY: Cambridge
STATE: Massachuse
                                                                                                                                                                                                            COUNTRY: US
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Search completed: Wed Apr 19 19:52:44 2000 Job time: 25 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 35.99 Seconds 329.759 Million cell updates/sec Wed Apr 19 19:50:05 2000; Run on:

ir output not generated

>US-09-297-092-1 (1-501) from US09297092.pep 3662 1 MRLPKLLTFLLWYLAWLDLE......ANNVVYKQYEDMVVESCGCR 501 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

188963 seqs, 23686106 residues Searched:

summaries Minimum Match 0% Listing first 45 Post-processing:

Database:

a-geneseq36 1:geneseqp

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

scale 0.220

Variance 166.724;

Mean 36.609;

Statistics:

SUMMARIES

	Description Pred. No.	TGF-beta superfamily s 0.00e+00		Human high mol. wt. pr 0.00e+00	bone morphogenic 0.	New TGF-beta family me 0.00e+00	Human MP52. 0.00e+00	Human MP52. 0.00e+00	Human TGF-beta protein 0.00e+00	Cartilage-derived morp 0.00e+00	Growth differentiation 9.21e-297	TGF-beta-like clone MP 2.39e-258	Cartilage-derived morp 2.00e-72	Human MP52 protein. 3.33e-69	Murine protein MP52. 3.33e-69	Human bone morphogenet 4.12e-69	Human mature VL-1 (BMP 4.12e-69	Human MP52 growth fact 7.77e-69	Human bone inducing fa 7.77e-69	Murine mV2 protein. 8.59e-65	Murine BMP-13 homologu 8.59e-65	1.	Human bone morphogenet 4.95e-61
SUMMAKIES	ID	W44868	W01799		W12770	R69600	W36100	W33008	W19210	R95635	R60022	R40800	R95636	W26590	R78731	W26591	R78730	W06920	W19846	R78739	W26595	R66867	R78734
	DB	н	-	-	-	Н	н	Н	Н	Н	Н	Н	Н	Н	-	Н	-1	н	7	Н	Н	-	Н
	Query Match Length DB	501	501	501	501	501	501	501	501	501	495	401	436	120	120	321	321	119	119	263	263	134	388
ф	Query Match	100.0	100.0	0.0	100.0	100.0	100.0	100.0	100.0	98.5	91.0	79.9	25.6	24.7	24.7	24.7	24.7	24.6	24.6	23.4	23.4	22.7	22.3
	Score	3662	3662	3662	3662	3662	3662	3662	3662	3608	3332	2925	939	904	904	903	903	900	006	856	856	832	815
	Result No.		7)	3	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22

3.36e-59	3.36e-59	2.90e-54	2.90e-54	2.90e-54	1.02e-53	1.92e-53	1.92e-53	9.58e-40	1.39e-37	5.91e-37	5.91e-37	5.91e-37	5.91e-37	5.91e-37	1.35e-36	1.35e-36	1.35e-3	1.35e-36	1.35e-36	1.35e-36	1.66e-36
BMP-2 propeptide/BMP-1	Fusion of BMP-2 propep	Bone morphogenetic pro	Human bone morphogenet	Human bone morphogenet	GDF-7 C-terminal regio	Murine BMP-12 homologu	Murine mV1 protein.	BMP2A/2B fusion protei	Prepro human CBMP2A .	Osteogenic protein CBM	Human osteogenic prote	Human osteogenic prote	Pre-pro-BMP2.	Human CBMP2A.	Human BMP-2A encoded b	Human bone morphogenic	Human pre-pro-BMP-2A.	Human BMP-2.	Human Bone Morphogenic	Human BMP-2A.	Pre-pro BMP5.
W26597	R78740	W54067	W26589	R78729	R65182	W26594	R78738	R15474	R51653	R44747	W44303	W89680	R47255	R85762	R14241	W24849	R29281	R36732	P80619	W15404	R47263
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411	411	129	294	294	161	240	240	400	396	386	396	396	396	396	386	386	396	396	396	396	453
21.7	21.7	20.2	20.2	20.2	20.1	20.0	20.0	15.9	15.2	15.0	15.0	15.0	15.0	15.0	14.9	14.9	14.9	14.9	14.9	14.9	14.9
795	795	741	741	741	735	732	732	581	557	550	550	250	550	550	546	546	546	546	546	546	545
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

QQ444mmmOL/L/L/DGGGGGG

ALIGNMENTS

Gaps ö Length 501; Score 3662; DB 1; Length 50 Pred. No. 0.00e+00; 0; Mismatches 0; Indels Query Match 100.0%; Best Local Similarity 100.0%; Matches 501; Conservative

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SDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR 240 181

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Pages 12-14; 21pp; German.

The present sequence is the human MP52 protein, which is described in W0 9316099 and 9504819 as a member of the human transforming growth factor beta superfamily. Active MP52 can be used in a medicament to treat and prevent nervous system diseases, and/or to treat neuropathological conditions caused by nervous
Medicaments contg. protein MP52 - useful for treating neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNFKNSAQLCLELEAWERGRAVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA
                                                                                                    RSGODDKTVYEYLFSQRRKRRAPLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIA
                                                                                                                                         PLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID
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                                                                                                                                                                                                                                                               Human MP52 protein.
Human; MP52; transforming growth factor; TGF; beta; medicament; treatment; prevention; nervous system; disease; neuropathology;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                              SANNVYKQYEDMVVESCGCR 501
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W01799 standard; Protein; 501
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                                                                                                                                                                                                                                                                                                                         18-JAN-1997.
12-JUL-1995; 025416.
12-JUL-1995; DE-025416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      501 AA;
                                                                                                                                                                                                                                                                                                   Homo sapiens.
DE19525416-A1.
                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; T59405
                                                                                                                                                                                                                                                                                                                                                                                                                                                            system ageing
                                                                                                                                                                                                                                                                                                                       16-JAN-1997
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Matches
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Done usesues 12.16; 25pp; Japanese. Claim 1; Page 12-16; 25pp; Japanese. Mal1900 is a high mol. wt. form of a human growth/differentiation factor MPS2. MPS2. promotes bone induction and is useful for plastic reconstructive surgery, cosmetic facial treatment, bone transplantation and tooth implantation. It is also useful for the treatment and prevention of disorders of bone formation, bone, cartilage, joint tissue, skin, mucous membranes, nails or teeth; for wound treatment and tissue skin, mucous membranes, nails or teeth; for wound treatment and tissue and in the standard of the skin mucous membranes.
                                                                                                                                                                                                 TVTPKGQLPGGKAPPKAGSVPSSFLLKKAREPGPPREPKEPFRPPPITPHEYMLSLYRTL 180
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360
                                                                                               420
                                                                                                                                                                                                                                                                     PLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID 480
                                                                                                                                                                                                                                                                                              Human high mol. wt. protéin MP52, a growth/differentiation factor. Growth factor; diferentiation; bone induction; osteoporosis; teeth; tooth; dental; joint tissue; cartilage; mucous membrane; skin; nails; wound healing; regeneration; skeletal disorder; fracture; dimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGHSYGGGATNANARAKGGTGQTGGLTQPKKDEPKKLPPRPGGPEPKPGHPPQTRQATAR 120
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                                                                        RNFKNSAQLCLELEAWERGRAVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA
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Pred. No. 0.00e+00;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-FEB-1997.
24-JUL-1996; JO2065.
24-JUL-1995; JP-218022.
(FARH ) HOECHST JAPAN LTD.
(FARH ) HOECHST PHARM & CHEM KK.
FUJINO Y, Kawai S, Kimura M, Mat
WPI: 97-132636/12.
N-PSDB; T61412.
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501; Conservative
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WO9704095-A1.
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New human bone morphogenic factor, MP52 Arg - used in the treatment of osteoporosis and bone fracture, and for promoting bone regrowth claim. Page 12-15; SOPP; English.

Novel human bone morphogenic factor MP52 Arg (W12770) is a growth factor that induces formation of cartilage from undifferentiated mesenchymal cells and which stimulates the differentiation and maturation of osteoblasts. It is effective for treating/preventing bone diseases caused by abnormal bone metabolism such as osteoporosis. It also accelerates the healing of bone fractures, and is useful for orthopaedic reconstruction, bone transplantation, and dental therapeutics because of its bone morphogenetic activity. It is also effective for preventing/treating cartilage, skin, connective tissue, mucous membrane, teeth and epithelial disorders.
                                                                                                                                                          360
                                              241 ILRKKPSDTAKPAAPGGGRAAOLKLSSCPSGROPASLLDVRSVPGLDGSGWEVFDIWKLF 300
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                               RNFKNSAQLCLELEAWERGRAVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA
                                                                                              RSGODDKTVYEYLFSQRRKRRAPLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant Mp52 Arg can be produced in host (e.g. CHO) cells utilising an isolated DNA sequence (T59729) in plasmid pMSS99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             381. 501
/label= Mat_protein
/note= "mature MP52 Arg preferred for use in
compsns. of the invention"
                                                                                                                                                                                                                                                                                                                                                                    Human bone morphogenic factor MP52 Arg.

Bone morphogenic factor; MF52 Arg; bone; cartilage; skin; connective Lissue; mucous membrane, epithelium; teeth; wound healing; vulnerary; tissue regeneration; osteoporosis; bone fracture; dental implant; osteoblast.
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Pred. No. 0.00e+00;
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Fujino Y, Kawai S, Kimura M, Matsumoto T, Takaha
WPI; 97-154261/14.
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/note= "alternative cleavage site 381. 501
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/label=_Sig_peptide
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Recombinant Mp52 Arg can be produce
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IT W12770 standard; Protein; 501
W12770;
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Matches 501; Concountry
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A BIOPPARM GES BIOTECHNOLOGISCHEN ENTWICKL.

Hotten G, Neidhardt H, Paulista M, Hoetten G;

NPI: 95-090897/12.

R PPSDB; 083695.

The according a new member of the TGF beta family - and related vectors, host cells etc., has mitogenic and relating or preventing diseases of bone and cartilage etc.

The amino acid sequence of a novel member of the transforming growth factor-beta (TGF-b) family named MP-52. The gene encodes a protein of 501 amino acids (AA). The protein, or at least the mature protein, of 501 amino acids (AA). The protein inducing properties useful in the treatment or prevention of diseases of bone, cartilage, connective tissue, skin, mucosa, epithelium or dental tissue. The protein can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             skin, mucosa, epithelium or dental tissue. The protein can also for wound healing and tissue regeneration e.g. in osteoporosis
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Transforming growth factor-beta family; mitogenic; differentiation;
treatment; prevention; disease; bone; cartilage; connective tissue;
skin; mucosa; epithelium; dental tissue; wound healing; osteoporosis;
GGHSYGGGATNANARAKGGTGQTGGLTQPKKDEPKKLPPRPGGPEPKPGHPPQTRQATAR 120
                 SDADRKGGNSSVKLEAGLANTITSFIDKGODDRGPVVRKORYVFDISALEKDGLLGAELR
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R69600 standard; Protein; 501
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16-FEB-1995.
09-AG-1994; E02630.
10-AUG-1993; DE-326829.
25-MAY-1994; DE-418222.
09-JUN-1994; DE-420157.
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Mature BMP can be produced by directly adding a BMP processing enzyme to a solution containing BMP precursor protein, or by transforming an animal cell with expression vectors containing DNA encoding the enzyme and precursor protein, culturing the encoding the mature BMP from the culture. The method can be used to produce MP52, BMP-2, BMP-4, BMP-6 and BMP-7, which can be used to treat bone formation or regeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Production of mature bone morphogenetic protein - by treatment of precursor protein with a processing enzyme such as furin either directly or by expressing them both in the same host Example 1; Pages 21-25; 34pp; Japanese.

The present sequence is MP52, which is a bone morphogenetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bone morphogenetic protein; BMP; processing enzyme; MP52;
BMP-2; BMP-4; BMP-6; BMP-7; bone formation; bone regeneration.
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                        0; Mismatches
           Pred. No.
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30-APR-1996; JP-130618.
(FARH ) HOECHST YAKUHIN KOGYO KK.
(FARH ) HOECHST PHARM & CHEM KK.
(FART) GARLST PHARM & CHEM KK.
WPI; 97-549748/50.
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W36100 standard; Protein; 501 AA.
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           Best Local Similarity 100.0%;
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Sequence 501 AA;
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WO9741250-A1.
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                                                                                                      60
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse anti-human MP52 monoclonal antibody - recognises the dimeric form of MP52 but not the monomer, and does not cross-react with TGF-beta or BMP-2
                                                                                      1 MRLPKLLTFLLWYLAWLDLEFICTVLGAPDLGQRPQGTRPGLAKAEAKERPPLARNVFRP
                                                                                                                                                                                                                                                                             181 SDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR
                                                                                                                                                                                                                                                                                               SDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR
                                                                                                                                                                                                                                                                                                                                             241 ILRKKPSDTAKPAAPGGGRAAQLKLSSCPSGRQPASLLDVRSVPGLDGSGWEVFDIWKLF
                                                                                                                                                                                                                                                                                                                                                              241 ILRKKPSDTAKPAPGGGRAAQLKLSSCPSGRQPASLLDVRSVPGLDGSGWEVFDIWKLF
                                                                                                                                                                                                                                                                                                                                                                                                                RNFKNSAQLCLELEAWERGRAVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSGQDDKTVYEYLFSQRRKRRAPLATRQGKRPSKNLKARCSRKALHVNFKDMGWDDWIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 PLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID
                                                                                                                                                                                                        121 TVTPKGQLPGGKAPPKAGSVPSSFLLKKAREPGPPREPKEPFRPPPITPHEYMLSLYRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Pages 31-35; 46pp; Japanese.

The present sequence, human MP52, was used in the preparation of a novel mouse monoclonal antibody (MAb), which recognises dimeric but not monomeric human MP52. The MAb has a heavy chain of subclass gamma, and does not cross-react with TGF_beta or BMP-2. The MAb may be used to purify and assay human
                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human MP52; mouse monoclonal antibody; MAb; purification;
 Score 3662; DB 1; Length 50
Pred. No. 0.00e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŝ
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13-MAY-1997; J01603.
07-MAY-1997; JP-131631.
13-MAY-1996; JP-141137.
(FARH ) HOECHST PHARM & CHEM KK.
J1tsukawa T, Kitagawa H, Nakagawa H, Yanagisawa
WPI; 98-008877/01.
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// abel = sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MP52, especially recombinant MP52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W33008 standard; Protein; 501 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 SANNVYKQYEDMVVESCGCR 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 SANNVVXKOYEDMVVESCGCR 501
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 501; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; T88340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human MP52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              assaying
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